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(54) Title: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS (54) Titre: METHODES PERMETTANT DE DIAGNOSTIQUER DU CANCER COLO-RECTAL, COMPOSITIONS, ET METHODES PERMETTANT DE DETECTER DES MODULATEURS DU CANCER COLO-RECTAL (57) Abstract <p>Described herein are methods that can be used for diagnosis and prognosis of colorectal cancer. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in colorectal and other cancers are described.</p> (57) Abrégé <p>L'invention concerne des méthodes utiles pour le diagnostic et le pronostic du cancer colo-rectal. L'invention concerne également des méthodes permettant de détecter la capacité que possèdent des agents bioactifs candidats pour moduler un cancer colo-rectal. L'invention concerne en outre des méthodes et des cibles moléculaires (gènes et leurs produits) permettant d'effectuer une intervention thérapeutique pour lutter contre le cancer colo-rectal et d'autres types cancers.</p>		

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(71) Applicant: EOS BIOTECHNOLOGY, INC. [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080-7019 (US).

(72) Inventors: MACK, David; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). GISH, Kurt, C.; 4302 23rd Street, San Francisco, CA 94114 (US). WILSON, Keith, E.; 219 Jeter Street, Redwood City, CA 94062 (US).

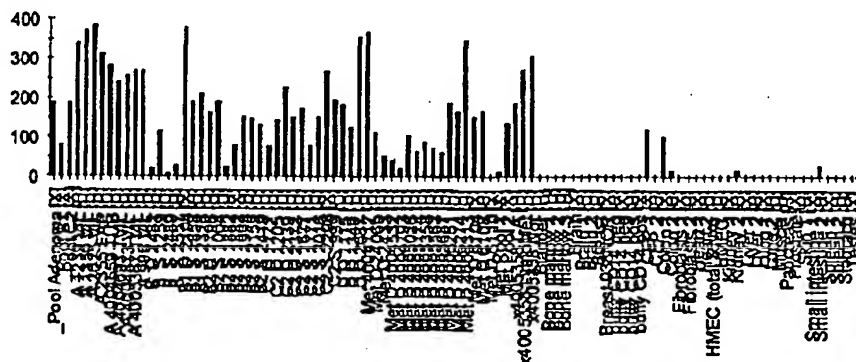
(74) Agents: BREZNER, David, J. et al.; Flehr Hohbach Test Albritton & Herbert LLP, Suite 3400, 4 Embarcadero Center, San Francisco, CA 94111-4187 (US).

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(54) Title: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS



(57) Abstract

Described herein are methods that can be used for diagnosis and prognosis of colorectal cancer. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in colorectal and other cancers are described.

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Description

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**NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS**

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FIELD OF THE INVENTION

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The invention relates to the identification of expression profiles and the nucleic acids involved in colorectal cancer, and to the use of such expression profiles and nucleic acids in diagnosis and prognosis of colorectal cancer. The invention further relates to methods for identifying and using candidate agents and/or targets which modulate colorectal cancer.

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BACKGROUND OF THE INVENTION

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Colorectal cancer is a significant cancer in Western populations. It develops as the result of a pathologic transformation of normal colon epithelium to an invasive cancer. There have been a number of recently characterized genetic alterations that have been implicated in colorectal cancer, including mutations in two classes of genes, tumor-suppressor genes and proto-oncogenes, with recent work suggesting that mutations in DNA repair genes may also be involved in tumorigenesis. For example, inactivating mutations of both alleles of the adenomatous polyposis coli (APC) gene, a tumor suppressor gene, appears to be one of the earliest events in colorectal cancer, and may even be the initiating event. Other genes implicated in colorectal cancer include the MCC gene, the p53 gene, the DCC (deleted in colorectal carcinoma) gene and other chromosome 18q genes, and genes in the TGF- β signaling pathway. For a review, see Molecular Biology of Colorectal Cancer, pp238-299, in Curr. Probl. Cancer, Sept/Oct 1997.

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majority of colorectal cancers but not in normal tissues. Liefers et al., New England J. of Med. 339(4):223 (1998).

Thus, methods that can be used for diagnosis and prognosis of colorectal cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of colorectal cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, provided herein are molecular targets for therapeutic intervention in colorectal and other cancers.

SUMMARY OF THE INVENTION

The present invention provides methods for screening for compositions which modulate colorectal cancer. Also provided herein are methods of inhibiting proliferation of cell, preferably a colorectal cancer cell. Methods of treatment of cancer, as well as compositions, are also provided herein.

In one aspect, a method of screening drug candidates comprises providing a cell that expresses an expression profile gene or fragments thereof. Preferred embodiments of the expression profile gene are genes which are differentially expressed in cancer cells, preferably colorectal cancer cells, compared to other cells. Preferred embodiments of expression profile genes used in the methods herein include but are not limited to the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9; fragments of the proteins of this group are also preferred. It is understood that molecules for use in the present invention may be from any figure or any subset of listed molecules. Therefore, for example, any one or more of the genes listed above can be used in the methods herein. In another embodiment, a nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

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Also provided herein is a method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), the method comprising combining the CCMP and a candidate bioactive agent, and determining the binding of the candidate agent to the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

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Further provided herein is a method for screening for a bioactive agent capable of modulating the activity of a CCMP. In one embodiment, the method comprises combining the CCMP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

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Also provided is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the CCMP, or an animal lacking the CCMP, for example as a result of a gene knockout.

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Additionally, provided herein is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual.

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Moreover, provided herein is a biochip comprising a nucleic acid segment which encodes a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably at least two nucleic acid segments are included. In another embodiment, the nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

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Furthermore, a method of diagnosing a disorder associated with colorectal cancer is provided. The method comprises determining the expression of a gene which encodes a colorectal cancer protein preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9 or a fragment thereof in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. A difference in the expression indicates that the first individual has a disorder associated with colorectal cancer.

In another aspect, the present invention provides an antibody which specifically binds to a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In a preferred embodiment, the fragment of CAA9 is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS. Other preferred fragments for the breast cancer proteins are shown in the figures. Preferably the antibody is a monoclonal antibody. The antibody can be a fragment of an antibody such as a single stranded antibody as further described herein, or can be conjugated to another molecule. In one embodiment, the antibody is a humanized antibody.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof. In a preferred embodiment, the method comprises combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said CCMP or fragment thereof. The method further includes determining the binding of said CCMP or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the antibody as well as the agent inhibits colorectal cancer.

In a further aspect, a method for inhibiting colorectal cancer is provided. In one embodiment, the method comprises administering to a cell a composition comprising an antibody to a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment

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thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method can be performed in vitro or in vivo, preferably in vivo to an individual. In a preferred embodiment the method of inhibiting colorectal cancer is provided to an individual with cancer. As described herein, methods of inhibiting colorectal cancer can be performed by administering an inhibitor of colorectal cancer protein activity, including antisense molecules, and preferably small molecules.

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Also provided herein are methods eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another aspect, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

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Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

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DETAILED DESCRIPTION OF THE FIGURES

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A method of neutralizing the effect of a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

In another aspect of the invention, a method of treating an individual for colorectal cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of CJA8. In another embodiment, the method comprises administering to a patient having colorectal cancer an antibody to CJA8 conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radiolotope.

Also provided herein is a method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

Novel sequences are also provided herein. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

Figure 1 provides the Accession numbers for genes, including expression sequence tags, (incorporated in their entirety here and throughout the application where Accession numbers are provided), upregulated in tumor tissue compared to normal colon tissue.

Figure 2 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 3 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 4 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

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Figure 5 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

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Figure 6 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

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5 Figure 7 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

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Figure 8 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

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Figure 9 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

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15 Figure 10 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

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Figure 11 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

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20 Figure 12 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

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Figure 13 provides the Accession numbers for genes or fragments thereof, including descriptions of the gene or encoded protein, upregulated in tumor tissue compared to normal colon tissue.

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25 Figure 14 provides a list of proteins, including Accession numbers for nucleic acid sequences associated with the encoding genes thereof, upregulated in tumor tissue compared to normal colon tissue.

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Figure 15 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal protein provided herein, CAA2. The start and stop codon are shaded. The sequence within the two cross marks indicates a preferred novel fragment of CAA2 provided herein, referred to herein as the "CAA2 5' end". Preferred embodiments of CAA2 include at least a portion of the CAA2 5'. The sequence in bold and indicated with a bar at the bottom right beginning with "GGC" and ending with "AAA" can be found in Accession no. AA505133.

Figure 16 shows an embodiment of a nucleic acid encoding CAA2, wherein the start and stop codons are shaded.

Figure 17 shows an embodiment of an amino acid sequence of CAA2. Preferred fragments include at least about 10 amino acids in the N-terminal end. The N-terminus as defined herein includes an embodiment beginning at the first amino acid until about any one of the three amino acids marked with a dot above them. In another embodiment, the N-terminus of CAA2 is defined as the amino acid sequence encoded by the CAA2 5' end.

Figure 18 shows the amino acid sequence of CAA2p1, a preferred CAA2 fragment provided herein.

Figure 19 shows the amino acid sequence of CAA2p2, a preferred CAA2 fragment provided herein.

Figure 20 shows an alignment of the human and mouse CAA2 polypeptides provided herein. The mouse polypeptide contains at least some of the sequence of each of the following Accession numbers: AA386837; AI508773; AA505293; and AA636546.

Figure 21 shows the relative amount of expression of CAA2 in various samples of colon cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 22 shows an embodiment of a colorectal cancer nucleic acid, CAA9 mRNA. The start and stop codons are underlined.

Figure 23 shows the open reading frame of the CAA9 gene wherein the start and stop codons are underlined.

Figure 24 shows an embodiment of the amino acid sequence of a colorectal cancer protein, CAA9, wherein putative transmembrane sequences are underlined. In one embodiment, CAA9 or fragments

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of CAA9 are soluble, therefore, the transmembrane domains are deleted, inactivated, and/or the peptide is truncated (with or without re-ligation) to form soluble CAA9.

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Figure 25 shows embodiments of colorectal cancer proteins (also termed colorectal cancer modulator proteins). Specifically, Figure 25 shows CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS and their respective solubilities.

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Figure 26 shows the relative amount of CAA9 expression in several different samples of colon cancer tissue (dark bars) and normal tissues (light bars).

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Figure 27 shows the nucleic acid sequence for the gene encoding CGA7. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA331393. Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

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Figures 28A and 28B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

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Figure 29 shows the amino acid sequence of CGA7.

Figures 30A and 30B show the relative expression of CGA7 in normal tissue and colon cancer tissue, respectively.

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Figure 31 shows the nucleic acid sequence for the mRNA encoding CGA8. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA2786503. Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

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Figures 32A and 32B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

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Figure 33 shows the amino acid sequence of CGA8.

Figure 34 shows the relative expression of CGA8 in breast cancer tissue, colon cancer tissue, normal tissue and fetal tissue.

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Figure 35 shows the sequence for the mRNA encoding CJA8. Start (ATG) and stop (TAA) codons are indicated by shaded boxes.

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Figure 36 shows the amino acid sequence for CJA8. A putative transmembrane region is designated by shading. A mouse homolog of this human protein is found at Accession Number AAF21308.1.

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5 Figure 37 shows the relative amount of expression of CJA8 in several different samples of colon tissues (dark bars) and normal tissues (light bars).

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Figure 38 shows the relative amount of expression of BCN7 in several different samples of colon tissues (dark bars) and normal tissues (light bars), as determined using the sequence of Accession Number N22107 as a probe.

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Figure 39 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, BCN7.

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Figure 40 shows the sequence for the mRNA encoding CZA8. Start (ATG) and stop (TGA) codons are indicated by underlining.

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Figure 41 shows the sequence for the mRNA encoding BCX2. Start (ATG) and stop (TGA) codons are indicated by underlining.

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Figure 42 shows the sequence for the mRNA encoding CBC2. Start (ATG) and stop (TAA) codons are indicated by underlining.

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Figure 44 shows the sequence for the mRNA encoding CBC3. Start (ATG) and stop (TGA) codons are indicated by underlining.

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Figure 45 shows the sequence for the mRNA encoding BCN5. Start (ATG) and stop (TAA) codons are indicated by underlining.

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Figure 46 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CJA9.

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Figure 47 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA1.

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Figure 48 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA2.

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DETAILED DESCRIPTION OF THE INVENTION

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The present invention provides novel methods for diagnosis and prognosis evaluation for colorectal cancer (CRC), as well as methods for screening for compositions which modulate CRC. In one aspect, the expression levels of genes are determined in different patient samples for which either diagnosis or prognosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from CRC tissue, and within CRC tissue, different prognosis states (good or poor long term survival prospects, for example) may be determined. By comparing expression profiles of colon tissue in known different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are differentially expressed in CRC versus normal colon tissue, as well as differential expression resulting in different prognostic outcomes, allows the use of this information in a number of ways. For example, the evaluation of a particular treatment regime may be evaluated: does a chemotherapeutic drug act to improve the long-term prognosis in a particular patient. Similarly, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the CRC expression profile or convert a poor prognosis profile to a better prognosis profile. This may be done by making biochips comprising sets of the important CRC genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the CRC proteins can be evaluated for diagnostic and prognostic purposes or to screen candidate agents. In addition, the CRC nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the CRC proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in colorectal cancer, CRC, herein termed "CRC sequences". As outlined below, CRC sequences include those that are up-regulated (i.e. expressed at a higher level) in CRC, as well as those that are down-regulated (i.e. expressed at a lower level) in CRC. In a preferred embodiment, the CRC sequences are from humans; however, as will be appreciated by those in the art, CRC sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other CRC sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). CRC sequences from other organisms may be obtained using the techniques outlined below.

CRC sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the CRC sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid by polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a CRC protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form

not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the CRC sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, CRC sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the CRC sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., *Tetrahedron* 49(10):1925 (1993) and references therein; Letsinger, *J. Org. Chem.* 35:3800 (1970); Sprinzl et al., *Eur. J. Biochem.* 81:579 (1977); Letsinger et al., *Nucl. Acids Res.* 14:3487 (1986); Sawai et al, *Chem. Lett.* 805 (1984), Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); and Pauwels et al., *Chemica Scripta* 26:141 (1986)), phosphorothioate (Mag et al., *Nucleic Acids Res.* 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., *J. Am. Chem. Soc.* 111:2321 (1989), O-methylphosphoramidite linkages (see Eckstein, *Oligonucleotides and Analogues: A Practical Approach*, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, *J. Am. Chem. Soc.* 114:1895 (1992); Meier et al., *Chem. Int. Ed. Engl.* 31:1008 (1992); Nielsen, *Nature*, 365:566 (1993); Carlsson et al., *Nature* 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., *Proc. Natl. Acad. Sci. USA* 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski et al., *Angew. Chem. Intl. Ed. English* 30:423 (1991); Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); Letsinger et al., *Nucleoside & Nucleotide* 13:1597 (1994); Chapters 2 and 3, *ASC Symposium Series* 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., *Bioorganic & Medicinal Chem. Lett.* 4:395 (1994); Jeffs et al., *J. Biomolecular NMR* 34:17 (1994); *Tetrahedron Lett.* 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, *ASC Symposium Series* 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., *Chem. Soc. Rev.* (1995) pp169-176). Several nucleic acid analogs are described in Rawls, *C & E News* June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

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As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

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5 Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

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15 The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand ("Watson") also defines the sequence of the other strand ("Crick"); thus the sequences described herein also includes the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

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25 A CRC sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

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30 The CRC sequences of the invention can be identified as follows. Samples of normal and tumor tissue are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are

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commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated, and the data analyzed.

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In a preferred embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the CRC screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is preferable that the target be disease specific, to minimize possible side effects.

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10 In a preferred embodiment, CRC sequences are those that are up-regulated in CRC; that is, the expression of these genes is higher in colorectal carcinoma as compared to normal colon tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby

15 expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. In addition, these genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, breast, kidney, prostate, small intestine and spleen.

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20 In a preferred embodiment, CRC sequences are those that are down-regulated in CRC; that is, the expression of these genes is lower in colorectal carcinoma as compared to normal colon tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

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25 CRC proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In a preferred embodiment the CRC protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, for example, signaling pathways); aberrant expression of such proteins results in unregulated or dysregulated cellular processes. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity

30 and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

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An increasingly appreciated concept in characterizing intracellular proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

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In a preferred embodiment, the CRC sequences are transmembrane proteins. Transmembrane proteins are molecules that span the phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

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Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Important transmembrane protein receptors include, but are not limited to insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor, etc.

Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid

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sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted.

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The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

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Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for example via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

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CRC proteins that are transmembrane are particularly preferred in the present invention as they are good targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities.

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It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, for example through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

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In a preferred embodiment, the CRC proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an

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endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. CRC proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, for example for blood tests.

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5 A CRC sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

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As used herein, a nucleic acid is a "CRC nucleic acid" if the overall homology of the nucleic acid sequence to the nucleic acid sequences encoding the amino acid sequences of the figures is preferably greater than about 75%, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. Homology in this context means sequence similarity or identity, with identity being preferred. A preferred comparison for homology purposes is to compare the sequence containing sequencing errors to the correct sequence. This homology will be determined using standard techniques known in the art, including, but not limited to, the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, PNAS USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by Devereux et al., Nucl. Acid Res. 12:387-395 (1984), preferably using the default settings, or by inspection.

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In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the figures, preferably those represented in Figure 12, more preferably those represented in Figures 13A and 13B, still more preferably those of Figures 14-20, 22-25, 27-29, 31-33, 35-37 and 39-48, and fragments thereof. In one embodiment the sequences utilized herein are those set forth in the figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the figures. In another embodiment, the sequences are sequence variants as further described herein.

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One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the

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clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, J. Mol. Evol. 35:351-360 (1987); the method is similar to that described by Higgins & Sharp CABIOS 5:151-153 (1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

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5 Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., J. Mol. Biol. 215, 403-410, (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., Methods in Enzymology, 266: 460-480 (1996); [http://blast.wustl.edu/blast/ REACRCE.html](http://blast.wustl.edu/blast/REACRCE.html)]. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

20 Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of the sequences of the figures. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

25 The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleosides than those of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

30 In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for example, nucleic acids which hybridize under high stringency to the nucleic acid sequences which encode the peptides identified in the figures, or their complements, are considered a CRC sequence. High stringency conditions are known in the art; see for example Maniatis et al., Molecular Cloning: A Laboratory Manual, 2d Edition, 1989, and Short Protocols in Molecular Biology, ed. Ausubel, et al.,

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both of which are hereby incorporated by reference. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g. 10 to 50 nucleotides) and at least about 60°C for long probes (e.g. greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

15 In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, *supra*, and Tijssen, *supra*.

In addition, the CRC nucleic acid sequences of the invention are fragments of larger genes, i.e. they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, additional sequences of the CRC genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Maniatis et al., and Ausubel, et al., *supra*, hereby expressly incorporated by reference.

25 Once the CRC nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire CRC nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant CRC nucleic acid can be further-used as a probe to identify and isolate other CRC nucleic acids, for example additional coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant CRC nucleic acids and proteins.

30 The CRC nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the CRC nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene

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therapy and/or antisense applications. Alternatively, the CRC nucleic acids that include coding regions of CRC proteins can be put into expression vectors for the expression of CRC proteins, again either for screening purposes or for administration to a patient.

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5 In a preferred embodiment, nucleic acid probes to CRC nucleic acids (both the nucleic acid sequences encoding peptides outlined in the figures and/or the complements thereof) are made. The
15 nucleic acid probes attached to the biochip are designed to be substantially complementary to the CRC nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be
20 perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by
25 "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double
30 stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being
35 particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping
40 probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid
45 support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be
50 covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent

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binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

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In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

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The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

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Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

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In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic

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acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

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In this embodiment, the oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

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In an additional embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

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Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

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In a preferred embodiment, CRC nucleic acids encoding CRC proteins are used to make a variety of expression vectors to express CRC proteins which can then be used in screening assays, as described below. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the CRC protein. The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

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Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the

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sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. The transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the CRC protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the CRC protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The CRC proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a CRC protein, under the appropriate conditions to

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induce or cause expression of the CRC protein. The conditions appropriate for CRC protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

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Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Drosophila melanogaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, THP1 cell line (a macrophage cell line) and human cells and cell lines.

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In a preferred embodiment, the CRC proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral systems. A preferred expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

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The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

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In a preferred embodiment, CRC proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can

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include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the CRC protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, CRC proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, CRC protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The CRC protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the CRC protein may be fused to a carrier protein to form an immunogen. Alternatively, the CRC protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the CRC protein is a CRC peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In one embodiment, the CRC nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or

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antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the CRC nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., *Nature*, **144**:945 (1962); David et al., *Biochemistry*, **13**:1014 (1974); Pain et al., *J. Immunol. Meth.*, **40**:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, **30**:407 (1982).

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10 Accordingly, the present invention also provides CRC protein sequences. A CRC protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the CRC protein has homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

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25 Also included within one embodiment of CRC proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques known in the art as are outlined above for the nucleic acid homologies.

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CRC proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of CRC proteins are portions or fragments of the wild type sequences. herein. In addition, as outlined above, the CRC

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nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

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In a preferred embodiment, the CRC proteins are derivative or variant CRC proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative CRC peptide will contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the CRC peptide.

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Also included in an embodiment of CRC proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the CRC protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant CRC protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the CRC protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

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While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed CRC variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of CRC protein activities.

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Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the

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molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the CRC protein are desired, substitutions are generally made in accordance with the following chart:

		Chart I	
		Original Residue	Exemplary Substitutions
15	10	Ala	Ser
		Arg	Lys
		Asn	Gln, His
20	15	Asp	Glu
		Cys	Ser
		Gln	Asn
25	20	Glu	Asp
		Gly	Pro
		His	Asn, Gln
30	25	Ile	Leu, Val
		Leu	Ile, Val
		Lys	Arg, Gln, Glu
35	30	Met	Leu, Ile
		Phe	Met, Leu, Tyr
		Ser	Thr
40	35	Thr	Ser
		Trp	Tyr
		Tyr	Trp, Phe
45	40	Val	Ile, Leu

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the CRC proteins as needed. Alternatively, the variant may be designed such that the biological activity of the CRC protein is altered. For example, glycosylation sites may be altered or removed.

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Covalent modifications of CRC polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a CRC polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of a CRC polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking CRC to a water-insoluble support matrix or surface for use in the method for purifying anti-CRC antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxy-succinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propionate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the CRC polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence CRC polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence CRC polypeptide.

Addition of glycosylation sites to CRC polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence CRC polypeptide (for O-linked glycosylation sites). The CRC amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the CRC polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the CRC polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

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Removal of carbohydrate moieties present on the CRC polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge et al., *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura et al., *Meth. Enzymol.*, 138:350 (1987).

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Another type of covalent modification of CRC comprises linking the CRC polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

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CRC polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a CRC polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a CRC polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the CRC polypeptide. The presence of such epitope-tagged forms of a CRC polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the CRC polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a CRC polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

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Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., *Mol. Cell. Biol.*, 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., *Molecular and Cellular Biology*, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., *Protein Engineering*, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., *BioTechnology*, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., *Science*, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., *J. Biol. Chem.*, 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., *Proc. Natl. Acad. Sci. USA*, 87:6393-6397 (1990)].

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Also included with the definition of CRC protein in one embodiment are other CRC proteins of the CRC family, and CRC proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related CRC proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the CRC nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

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In addition, as is outlined herein, CRC proteins can be made that are longer than those depicted in the figures, for example, by the elucidation of additional sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

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CRC proteins may also be identified as being encoded by CRC nucleic acids. Thus, CRC proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

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In a preferred embodiment, when the CRC protein is to be used to generate antibodies, for example for immunotherapy, the CRC protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller CRC protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from CAA2p1 and CAA2p2. In another preferred embodiment, the epitope is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA89p5 and CAA9p5MAPS.

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In one embodiment, the term "antibody" includes antibody fragments, as are known in the art, including Fab, Fab₂, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies.

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Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the CAA2 or

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fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include the CAA2 polypeptide or fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for a CRC protein or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific.

In a preferred embodiment, the antibodies to CRC are capable of reducing or eliminating the biological function of CRC, as is described below. That is, the addition of anti-CRC antibodies (either polyclonal or preferably monoclonal) to CRC (or cells containing CRC) may reduce or eliminate the CRC activity.

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Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

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In a preferred embodiment the antibodies to the CRC proteins are humanized antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

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Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

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Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*,

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222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology 10, 779-783 (1992); Lonberg et al., Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

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By immunotherapy is meant treatment of CRC with an antibody raised against CRC proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen.

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In a preferred embodiment the CRC proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted CRC protein.

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In another preferred embodiment, the CRC protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the CRC protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane CRC protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the CRC protein. The antibody is also an antagonist of the CRC protein. Further, the antibody prevents activation of the transmembrane CRC protein. In one aspect, when the antibody prevents the binding of other molecules to the CRC protein, the antibody prevents growth of the cell. The antibody also sensitizes

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the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity. Thus, CRC is treated by administering to a patient antibodies directed against the transmembrane CRC protein.

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In another preferred embodiment, the antibody is conjugated to a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the CRC protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the CRC protein. The therapeutic moiety may inhibit enzymatic activity such as protease or protein kinase activity associated with CRC.

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In a preferred embodiment, the therapeutic moiety may also be a cytotoxic agent. In this method, targeting the cytotoxic agent to tumor tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with CRC. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins.

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Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against CRC proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane CRC proteins not only serves to increase the local concentration of therapeutic moiety in the CRC afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

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In another preferred embodiment, the CRC protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the CRC protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

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The CRC antibodies of the invention specifically bind to CRC proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least 10^4 - 10^6 M^{-1} , with a preferred range being 10^7 - 10^9 M^{-1} .

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In a preferred embodiment, the CRC protein is purified or isolated after expression. CRC proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the CRC protein may be purified using a standard anti-CRC antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the CRC protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the CRC proteins and nucleic acids are useful in a number of applications.

In one aspect, the expression levels of genes are determined for different cellular states in the CRC phenotype; that is, the expression levels of genes in normal colon tissue and in CRC tissue (and in some cases, for varying severities of CRC that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be done or confirmed: does tissue from a particular patient have the gene expression profile of normal or CRC tissue.

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes' temporal and/or cellular expression patterns within and among the cells. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, for example, normal versus CRC tissue. That is, genes may be turned on or turned off in a particular state, relative to another state. As is apparent to the skilled artisan, any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques in one such state or cell type, but is not detectable in both. Alternatively, the determination is quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard

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characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e. upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

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As will be appreciated by those in the art, this may be done by evaluation at either the gene transcript, or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Thus, the proteins corresponding to CRC genes, i.e. those identified as being important in a CRC phenotype, can be evaluated in a CRC diagnostic test.

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In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well. Similarly, these assays may be done on an individual basis as well.

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In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below in the example.

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In a preferred embodiment nucleic acids encoding the CRC protein are detected. Although DNA or RNA encoding the CRC protein may be detected, of particular interest are methods wherein the mRNA encoding a CRC protein is detected. The presence of mRNA in a sample is an indication that the CRC gene has been transcribed to form the mRNA, and suggests that the protein is expressed. Probes to detect the mRNA can be any nucleotide/deoxynucleotide probe that is complementary to and base pairs with the mRNA and includes but is not limited to oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled

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nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a CRC protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

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In a preferred embodiment, any of the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in diagnostic assays. This can be done on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

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As described and defined herein, CRC proteins, including intracellular, transmembrane or secreted proteins, find use as markers of CRC. Detection of these proteins in putative CRC tissue or patients allows for a determination or diagnosis of CRC. Numerous methods known to those of ordinary skill in the art find use in detecting CRC. In one embodiment, antibodies are used to detect CRC proteins. A preferred method separates proteins from a sample or patient by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be any other type of gel including isoelectric focusing gels and the like). Following separation of proteins, the CRC protein is detected by immunoblotting with antibodies raised against the CRC protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

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In another preferred method, antibodies to the CRC protein find use in in situ imaging techniques. In this method cells are contacted with from one to many antibodies to the CRC protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the CRC protein(s) contains a detectable label. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of CRC proteins. As will be appreciated by one of ordinary skill in the art, numerous other histological imaging techniques are useful in the invention.

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In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

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In another preferred embodiment, antibodies find use in diagnosing CRC from blood samples. As previously described, certain CRC proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted CRC proteins. Antibodies can be used to detect the CRC by any of the previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like, as will be appreciated by one of ordinary skill in the art.

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In a preferred embodiment, in situ hybridization of labeled CRC nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including CRC tissue and/or normal tissue, are made. In situ hybridization as is known in the art can then be done.

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It is understood that when comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis as well as a prognosis. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis.

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In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to CRC severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, the CRC probes are attached to biochips for the detection and quantification of CRC sequences in a tissue or patient. The assays proceed as outlined for diagnosis.

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In a preferred embodiment, any of the three classes of proteins as described herein are used in drug screening assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, Zlokarnik, et al., Science 279, 84-8 (1998), Heid, 1996 #69.

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In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified CRC proteins are used in screening assays. That is, the present

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invention provides novel methods for screening for compositions which modulate the CRC phenotype. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

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Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in CRC, candidate bioactive agents may be screened to modulate this gene's response; preferably to down regulate the gene, although in some circumstances to up regulate the gene. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tumor tissue, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4 fold increase in tumor compared to normal tissue, a decrease of about four fold is desired; a 10 fold decrease in tumor compared to normal tissue gives a 10 fold increase in expression for a candidate agent is desired.

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As will be appreciated by those in the art, this may be done by evaluation at either the gene or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays.

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In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well.

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In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below.

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Generally, in a preferred embodiment, a candidate bioactive agent is added to the cells prior to analysis. Moreover, screens are provided to identify a candidate bioactive agent which modulates colorectal cancer, modulates CRC proteins, binds to a CRC protein, or interferes between the binding of a CRC protein and an antibody.

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The term "candidate bioactive agent" or "drug candidate" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for bioactive agents that are capable of directly or indirectly altering either the CRC phenotype or the expression of a CRC sequence, including both nucleic acid sequences and protein sequences. In preferred embodiments, the bioactive agents modulate the expression profiles, or expression profile nucleic acids or proteins provided herein. In a particularly preferred embodiment, the candidate agent suppresses a CRC phenotype, for example to a normal colon tissue fingerprint. Similarly, the candidate agent preferably suppresses a severe CRC phenotype. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a candidate agent will neutralize the effect of a CRC protein. By "neutralize" is meant that activity of a protein is either inhibited or counter acted against so as to have substantially no effect on a cell.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random

chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

In a preferred embodiment, the candidate bioactive agents are proteins. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and noreleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

In a preferred embodiment, the candidate bioactive agents are naturally occurring proteins or fragments of naturally occurring proteins. Thus, for example, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of procaryotic and eucaryotic proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred.

In a preferred embodiment, the candidate bioactive agents are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a

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defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

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5 In a preferred embodiment, the candidate bioactive agents are nucleic acids, as defined above.

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As described above generally for proteins, nucleic acid candidate bioactive agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

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In a preferred embodiment, the candidate bioactive agents are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing the target sequences to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR occurring as needed, as will be appreciated by those in the art. For example, an in vitro transcription with labels covalently attached to the nucleosides is done. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

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In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. As known in the art, unbound labeled streptavidin is removed prior to analysis.

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As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670,

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5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

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5 A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

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These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

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1.5 The reactions outlined herein may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target.

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Once the assay is run, the data is analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

2.5 The screens are done to identify drugs or bioactive agents that modulate the CRC phenotype. Specifically, there are several types of screens that can be run. A preferred embodiment is in the screening of candidate agents that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. That is, candidate agents that can mimic or produce an expression profile in CRC similar to the expression profile of normal colon tissue is expected to result in a suppression of the CRC phenotype. Thus, in this embodiment, mimicking an expression profile, or changing one profile to another, is the goal.

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In a preferred embodiment, as for the diagnosis and prognosis applications, having identified the differentially expressed genes important in any one state, screens can be run to alter the expression of the genes individually. That is, screening for modulation of regulation of expression of a single gene can be done; that is, rather than try to mimic all or part of an expression profile, screening for regulation of individual genes can be done. Thus, for example, particularly in the case of target genes whose presence or absence is unique between two states, screening is done for modulators of the target gene expression.

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In a preferred embodiment, screening is done to alter the biological function of the expression product of the differentially expressed gene. Again, having identified the importance of a gene in a particular state, screening for agents that bind and/or modulate the biological activity of the gene product can be run as is more fully outlined below.

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Thus, screening of candidate agents that modulate the CRC phenotype either at the gene expression level or the protein level can be done.

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In addition screens can be done for novel genes that are induced in response to a candidate agent. After identifying a candidate agent based upon its ability to suppress a CRC expression pattern leading to a normal expression pattern, or modulate a single CRC gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated CRC tissue reveals genes that are not expressed in normal tissue or CRC tissue, but are expressed in agent treated tissue. These agent specific sequences can be identified and used by any of the methods described herein for CRC genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated CRC tissue sample.

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Thus, in one embodiment, a candidate agent is administered to a population of CRC cells, that thus has an associated CRC expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e. a peptide) may be put into a viral construct such as a retroviral construct and added to the cell, such that expression of the peptide agent is accomplished; see PCT US97/01019, hereby expressly incorporated by reference.

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Once the candidate agent has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

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Thus, for example, CRC tissue may be screened for agents that reduce or suppress the CRC phenotype. A change in at least one gene of the expression profile indicates that the agent has an effect on CRC activity. By defining such a signature for the CRC phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

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In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "CRC proteins" or a "CCMP". In preferred embodiments, the CCMP is as depicted in Figures 17-20, 24, 25, 29, 33 and 36, more preferably the protein having the sequence shown in Figures 29 or 36 or encoded by the sequences of Figures 27, 36 and 39-48. The CCMP may be a fragment, or alternatively, be the full length protein to a fragment shown herein. Preferably, the CCMP is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment.

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In a preferred embodiment, the fragment is from CAA9. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the CAA9 fragment has an N-terminal Cys to aid in solubility. Preferably, the fragment is selected from CAA9p1, Caa9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.

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In a preferred embodiment, the fragment is charged and from the c-terminus of CAA2. In one embodiment, the c-terminus of the fragment is kept as a free acid and the n-terminus is a free amine to aid in coupling, i.e., to cysteine. In another embodiment, the fragment is an internal peptide overlapping hydrophilic stretch of CAA2. In a preferred embodiment, the termini is blocked. Preferably, the fragment of CAA2 is selected from CAA2p1 or CAA2p2. In another preferred embodiment, the fragment is a novel fragment from the N-terminal. In one embodiment, the fragment excludes sequence outside of the N-terminal, in another embodiment, the fragment includes at least a portion of the N-terminal. "N-terminal" is used interchangeably herein with "N-terminus" which is further described above.

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In one embodiment the CRC proteins are conjugated to an immunogenic agent as discussed herein.
In one embodiment the CRC protein is conjugated to BSA.

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Thus, in a preferred embodiment, screening for modulators of expression of specific genes can be done. This will be done as outlined above, but in general the expression of only one or a few genes are evaluated.

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In a preferred embodiment, screens are designed to first find candidate agents that can bind to differentially expressed proteins, and then these agents may be used in assays that evaluate the ability of the candidate agent to modulate differentially expressed activity. Thus, as will be appreciated by those in the art, there are a number of different assays which may be run; binding assays and activity assays.

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In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. In general, this is done as is known in the art. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the CRC proteins can be used in the assays.

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Thus, in a preferred embodiment, the methods comprise combining a CRC protein and a candidate bioactive agent, and determining the binding of the candidate agent to the CRC protein. Preferred embodiments utilize the human CRC protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative CRC proteins may be used.

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Generally, in a preferred embodiment of the methods herein, the CRC protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the

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composition and is nondiffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

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In a preferred embodiment, the CRC protein is bound to the support, and a candidate bioactive agent is added to the assay. Alternatively, the candidate agent is bound to the support and the CRC protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

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The determination of the binding of the candidate bioactive agent to the CRC protein may be done in a number of ways. In a preferred embodiment, the candidate bioactive agent is labeled, and binding determined directly. For example, this may be done by attaching all or a portion of the CRC protein to a solid support, adding a labeled candidate agent (for example a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as is known in the art.

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By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

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In some embodiments, only one of the components is labeled. For example, the proteins (or proteinaceous candidate agents) may be labeled at tyrosine positions using ^{125}I , or with fluorophores. Alternatively, more than one component may be labeled with different labels; using ^{125}I for the proteins, for example, and a fluorophor for the candidate agents.

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In a preferred embodiment, the binding of the candidate bioactive agent is determined through the use of competitive binding assays. In this embodiment, the competitor is a binding moiety known to bind to the target molecule (i.e. CRC), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding as between the bioactive agent and the binding moiety, with the binding moiety displacing the bioactive agent.

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In one embodiment, the candidate bioactive agent is labeled. Either the candidate bioactive agent, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high through put screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

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In a preferred embodiment, the competitor is added first, followed by the candidate bioactive agent. Displacement of the competitor is an indication that the candidate bioactive agent is binding to the CRC protein and thus is capable of binding to, and potentially modulating, the activity of the CRC protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the candidate bioactive agent is labeled, the presence of the label on the support indicates displacement.

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In an alternative embodiment, the candidate bioactive agent is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the bioactive agent is bound to the CRC protein with a higher affinity. Thus, if the candidate bioactive agent is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the candidate agent is capable of binding to the CRC protein.

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In a preferred embodiment, the methods comprise differential screening to identify bioactive agents that are capable of modulating the activity of the CRC proteins. In this embodiment, the methods comprise combining a CRC protein and a competitor in a first sample. A second sample comprises a candidate bioactive agent, a CRC protein and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the CRC protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the CRC protein.

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Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native CRC protein, but cannot bind to modified CRC proteins. The structure of the CRC protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect CRC bioactivity are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

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Positive controls and negative controls may be used in the assays. Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, all samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

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A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding.

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Screening for agents that modulate the activity of CRC proteins may also be done. In a preferred embodiment, methods for screening for a bioactive agent capable of modulating the activity of CRC proteins comprise the steps of adding a candidate bioactive agent to a sample of CRC proteins, as above, and determining an alteration in the biological activity of CRC proteins. "Modulating the activity of CRC" includes an increase in activity, a decrease in activity, or a change in the type or kind of activity present. Thus, in this embodiment, the candidate agent should both bind to CRC proteins (although this may not be necessary), and alter its biological or biochemical activity as defined herein.

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The methods include both in vitro screening methods, as are generally outlined above, and in vivo screening of cells for alterations in the presence, distribution, activity or amount of CRC proteins.

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Thus, in this embodiment, the methods comprise combining a CRC sample and a candidate bioactive agent, and evaluating the effect on CRC activity. By "CRC activity" or grammatical equivalents herein is meant one of the CRC's biological activities, including, but not limited to, cell division, preferably in colon tissue, cell proliferation, tumor growth, transformation of cells. In one embodiment, CRC activity includes activation of CZA8, BCX2, CBC2, CBC1, CBC3, CJA9, BCN5, CQA1, BCN7, CQA2, CJA8,

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CAA2, CAA9, CGA7 and/or CGA8", preferably one of the CRC proteins listed in Figure 14. An inhibitor of CRC activity is the inhibition of any one or more CRC activities.

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In a preferred embodiment, the activity of the CRC protein is increased; in another preferred embodiment, the activity of the CRC protein is decreased. Thus, bioactive agents that are antagonists are preferred in some embodiments, and bioactive agents that are agonists may be preferred in other embodiments.

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In a preferred embodiment, the invention provides methods for screening for bioactive agents capable of modulating the activity of a CRC protein. The methods comprise adding a candidate bioactive agent, as defined above, to a cell comprising CRC proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a CRC protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

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In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

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In this way, bioactive agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the CRC protein. In one embodiment, "colorectal cancer protein activity" as used herein includes at least one of the following: colorectal cancer activity, binding to CJA8, activation of CJA8 or activation of substrates of CJA8 by CJA8. In one embodiment, colorectal cancer activity is defined as the unregulated proliferation of colon tissue, or the growth of cancer in colon tissue. In one aspect, colorectal cancer activity as defined herein is related to the activity of CJA8 in the upregulation of CJA8 in colon cancer tissue.

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In another embodiment, colorectal cancer protein activity includes at least one of the following: colorectal cancer activity, binding to one of CAA2, CAA9, CGA7 and CGA8, activation of one of CAA2, CAA9, CGA7, and CGA8 or activation of substrates of CAA2, CAA9, CGA7 or CGA8 by CAA2, CAA9, CGA7 or CGA8, respectively. In one preferred embodiment, CAA2 comprises its N-terminal end. In one aspect, colorectal cancer activity as defined herein is related to the activity of CAA2, CAA9, CGA7 and/or CGA8 in the upregulation of CAA2, CAA9, CGA7 and/or CGA8, respectively, in colon cancer tissue.

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In one embodiment, a method of inhibiting colon cancer cell division is provided. The method comprises administration of a colorectal cancer inhibitor.

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In another embodiment, a method of inhibiting tumor growth is provided. The method comprises administration of a colorectal cancer inhibitor.

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5 In a further embodiment, methods of treating cells or individuals with cancer are provided. The method comprises administration of a colorectal cancer inhibitor.

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In one embodiment, a colorectal cancer inhibitor is an antibody as discussed above. In another embodiment, the colorectal cancer inhibitor is an antisense molecule. Antisense molecules as used herein include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for colorectal cancer molecules. A preferred antisense molecule is for CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, BCN5, CQA1, BCN7, CQA2, CAA2, CAA9, CGA7 or CGA8, more preferably for the CRC sequences referenced in Figure 14, or for a ligand or activator thereof. A most preferred antisense molecule is for CJA8 or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

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20 Antisense molecules may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

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30 The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host, as previously described. The agents may be administered in a variety of

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ways, orally, parenterally e.g., subcutaneously, intraperitoneally, intravascularly, etc. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt.%. The agents may be administered alone or in combination with other treatments, i.e., radiation.

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5 The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

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Without being bound by theory, it appears that the various CRC sequences are important in CRC. Accordingly, disorders based on mutant or variant CRC genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant CRC genes comprising determining all or part of the sequence of at least one endogenous CRC genes in a cell. As will be appreciated by those in the art, this may be done using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the CRC genotype of an individual comprising determining all or part of the sequence of at least one CRC gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced CRC gene to a known CRC gene, i.e. a wild-type gene.

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The sequence of all or part of the CRC gene can then be compared to the sequence of a known CRC gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the CRC gene of the patient and the known CRC gene is indicative of a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the CRC genes are used as probes to determine the number of copies of the CRC gene in the genome.

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In another preferred embodiment CRC genes are used as probed to determine the chromosomal localization of the CRC genes. Information such as chromosomal localization finds use in providing a

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diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in CRC gene loci.

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Thus, in one embodiment, methods of modulating CRC in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-CRC antibody that reduces or eliminates the biological activity of an endogeneous CRC protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a CRC protein. As will be appreciated by those in the art, this may be accomplished in any number of ways. In a preferred embodiment, for example when the CRC sequence is down-regulated in CRC, the activity of the CRC gene is increased by increasing the amount of CRC in the cell, for example by overexpressing the endogeneous CRC or by administering a gene encoding the CRC sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the endogeneous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, for example when the CRC sequence is up-regulated in CRC, the activity of the endogeneous CRC gene is decreased, for example by the administration of a CRC antisense nucleic acid.

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In one embodiment, the CRC proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to CRC proteins, which are useful as described herein. Similarly, the CRC proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify CRC antibodies. In a preferred embodiment, the antibodies are generated to epitopes unique to a CRC protein; that is, the antibodies show little or no cross-reactivity to other proteins. These antibodies find use in a number of applications. For example, the CRC antibodies may be coupled to standard affinity chromatography columns and used to purify CRC proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the CRC protein.

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In one embodiment, a therapeutically effective dose of a CRC or modulator thereof is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art, adjustments for CRC degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

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A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals, and organisms. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, and in the most preferred embodiment the patient is human.

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5 The administration of the CRC proteins and modulators of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the CRC proteins and modulators may be directly applied as a solution or spray.

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10 The pharmaceutical compositions of the present invention comprise a CRC protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

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The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol. Additives are well known in the art, and are used in a variety of formulations.

In a preferred embodiment, CRC proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, CRC genes (including both the full-length

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sequence, partial sequences, or regulatory sequences of the CRC coding regions) can be administered in gene therapy applications, as is known in the art. These CRC genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

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5 In a preferred embodiment, CRC genes are administered as DNA vaccines, either single genes or combinations of CRC genes. Naked DNA vaccines are generally known in the art. Brower, Nature Biotechnology, 16:1304-1305 (1998).

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In one embodiment, CRC genes of the present invention are used as DNA vaccines. Methods for the use of genes as DNA vaccines are well known to one of ordinary skill in the art, and include placing a CRC gene or portion of a CRC gene under the control of a promoter for expression in a CRC patient. The CRC gene used for DNA vaccines can encode full-length CRC proteins, but more preferably encodes portions of the CRC proteins including peptides derived from the CRC protein. In a preferred embodiment a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a CRC gene. Similarly, it is possible to immunize a patient with a plurality of CRC genes or portions thereof as defined herein. Without being bound by theory, expression of the polypeptide encoded by the DNA vaccine, cytotoxic T-cells, helper T-cells and antibodies are induced which recognize and destroy or eliminate cells expressing CRC proteins.

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In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the CRC polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are known to those of ordinary skill in the art and find use in the invention.

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In another preferred embodiment CRC genes find use in generating animal models of CRC. As is appreciated by one of ordinary skill in the art, when the CRC gene identified is repressed or diminished in CRC tissue, gene therapy technology wherein antisense RNA directed to the CRC gene will also diminish or repress expression of the gene. An animal generated as such serves as an animal model of CRC that finds use in screening bioactive drug candidates. Similarly, gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the CRC protein. When desired, tissue-specific expression or knockout of the CRC protein may be necessary.

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It is also possible that the CRC protein is overexpressed in CRC. As such, transgenic animals can be generated that overexpress the CRC protein. Depending on the desired expression level, promoters

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of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of CRC and are additionally useful in screening for bioactive molecules to treat CRC.

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5 It is understood that the examples described herein in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references and sequences of accession numbers cited herein are incorporated by reference in their entirety.

EXAMPLES

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Example 1

10 Tissue Preparation, Labeling Chips, and Fingerprints

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Purify total RNA from tissue using TRIzol Reagent

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15 Estimate tissue weight. Homogenize tissue samples in 1ml of TRIzol per 50mg of tissue using a Polytron 3100 homogenizer. The generator/probe used depends upon the tissue size. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. Use the 20mm generator for tissue weighing more than 0.6g. If the working volume is greater than 2ml, then homogenize tissue in a 15ml polypropylene tube (Falcon 2059). Fill tube no greater than 10ml.

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HOMOGENIZATION

20 Before using generator, it should have been cleaned after last usage by running it through soapy H₂O and rinsing thoroughly. Run through with EtOH to sterilize. Keep tissue frozen until ready. Add TRIzol directly to frozen tissue then homogenize.

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Following homogenization, remove insoluble material from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. Transfer the cleared homogenate to a new tube(s). The samples may be frozen now at -60 to -70°C (and kept for at least one month) or you may continue with the purification.

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PHASE SEPARATION

Incubate the homogenized samples for 5 minutes at room temperature.

Add 0.2ml of chloroform per 1ml of TRIzol reagent used in the original homogenization.

Cap tubes securely and shake tubes vigorously by hand (do not vortex) for 15 seconds.

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Incubate samples at room temp. for 2-3 minutes. Centrifuge samples at 6500rpm in a Sorvall superspeed for 30 min. at 4°C. (You may spin at up to 12,000 x g for 10 min. but you risk breaking your tubes in the centrifuge.)

RNA PRECIPITATION

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- 5 Transfer the aqueous phase to a fresh tube. Save the organic phase if isolation of DNA or protein is desired. Add 0.5ml of isopropyl alcohol per 1ml of TRIzol reagent used in the original homogenization. Cap tubes securely and invert to mix. Incubate samples at room temp. for 10 minutes. Centrifuge samples at 6500rpm in Sorvall for 20min. at 4°C.

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RNA WASH

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- 10 Pour off the supernate. Wash pellet with cold 75% ethanol. Use 1ml of 75% ethanol per 1ml of TRIzol reagent used in the initial homogenization. Cap tubes securely and invert several times to loosen pellet. (Do not vortex). Centrifuge at <8000rpm (<7500 x g) for 5 minutes at 4°C. Pour off the wash. Carefully transfer pellet to an eppendorf tube (let it slide down the tube into the new tube and use a pipet tip to help guide it in if necessary). Depending on the volumes you are working with, you can decide what size tube(s) you want to precipitate the RNA in. When I tried leaving the RNA in the large 15ml tube, it took so long to dry (i.e. it did not dry) that I eventually had to transfer it to a smaller tube. Let pellet dry in hood. Resuspend RNA in an appropriate volume of DEPC H₂O. Try for 2-5ug/ul. Take absorbance readings.

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Purify poly A⁺ mRNA from total RNA or clean up total RNA with Qiagen's

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RNeasy kit

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- 20 Purification of poly A⁺ mRNA from total RNA. Heat oligotex suspension to 37°C and mix immediately before adding to RNA. Incubate Elution Buffer at 70°C. Warm up 2 x Binding Buffer at 65°C if there is precipitate in the buffer. Mix total RNA with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook. Incubate for 3 minutes at 65°C. Incubate for 10 minutes at room temperature.

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Centrifuge for 2 minutes at 14,000 to 18,000 g. If centrifuge has a "soft setting," then use it. Remove supernatant without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. Save sup until certain that satisfactory binding and elution of poly A⁺ mRNA has occurred.

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- 30 Gently resuspend in Wash Buffer OW2 and pipet onto spin column. Centrifuge the spin column at full speed (soft setting if possible) for 1 minute.

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Transfer spin column to a new collection tube and gently resuspend in Wash Buffer OW2 and centrifuge as describe herein.

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Transfer spin column to a new tube and elute with 20 to 100 ul of preheated (70°C) Elution Buffer. Gently resuspend Oligotex resin by pipetting up and down. Centrifuge as above. Repeat elution with fresh elution buffer or use first eluate to keep the elution volume low.

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Read absorbance, using diluted Elution Buffer as the blank.

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Before proceeding with cDNA synthesis, the mRNA must be precipitated. Some component leftover or in the Elution Buffer from the Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA.

10 Ethanol Precipitation

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Add 0.4 vol. of 7.5 M NH_4OAc + 2.5 vol. of cold 100% ethanol. Precipitate at -20°C 1 hour to overnight (or 20-30 min. at -70°C). Centrifuge at 14,000-16,000 x g for 30 minutes at 4°C. Wash pellet with 0.5ml of 80% ethanol (-20°C) then centrifuge at 14,000-16,000 x g for 5 minutes at room temperature. Repeat 80% ethanol wash. Dry the last bit of ethanol from the pellet in the hood. (Do not speed vacuum). Suspend pellet in DEPC H_2O at 1ug/ul concentration.

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Clean up total RNA using Qiagen's RNeasy kit

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Add no more than 100ug to an RNeasy column. Adjust sample to a volume of 100ul with RNase-free water. Add 350ul Buffer RLT then 250ul ethanol (100%) to the sample. Mix by pipetting (do not centrifuge) then apply sample to an RNeasy mini spin column. Centrifuge for 15 sec at

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>10,000rpm. If concerned about yield, re-apply flowthrough to column and centrifuge again.

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Transfer column to a new 2-ml collection tube. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough then centrifuge for 2 min at maximum speed to dry column membrane. Transfer column to a new 1.5-ml collection tube and apply 30-50ul of RNase-free water directly onto column membrane. Centrifuge 1 min at >10,000rpm. Repeat elution. Take absorbance reading. If necessary, ethanol precipitate with ammonium acetate and 2.5X volume 100% ethanol.

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Make cDNA using Gibco's "SuperScript Choice System for cDNA Synthesis" kit First Strand cDNA Synthesis

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Use 5ug of total RNA or 1ug of polyA+ mRNA as starting material. For total RNA, use 2ul of SuperScript RT. For polyA+ mRNA, use 1ul of SuperScript RT. Final volume of first strand synthesis mix is 20ul. RNA must be in a volume no greater than 10ul. Incubate RNA with 1ul of 100pmol T7-T24 oligo for 10 min at 70C. On ice, add 7 ul of: 4ul 5X 1st Strand Buffer, 2ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. Incubate at 37C for 2 min then add SuperScript RT. Incubate at 37C for 1 hour.

Second Strand Synthesis

Place 1st strand reactions on ice.

Add: 91ul DEPC H2O
30ul 5X 2nd Strand Buffer
3ul 10mM dNTP mix
1ul 10U/ul *E.coli* DNA Ligase
4ul 10U/ul *E.coli* DNA Polymerase
1ul 2U/ul RNase H

Make the above into a mix if there are more than 2 samples. Mix and incubate 2 hours at 16C. Add 2ul T4 DNA Polymerase. Incubate 5 min at 16C. Add 10ul of 0.5M EDTA

Clean up cDNA

Phenol:Chloroform:Isoamyl Alcohol (25:24:1) purification using Phase-Lock gel tubes:

Centrifuge PLG tubes for 30 sec at maximum speed. Transfer cDNA mix to PLG tube. Add equal volume of phenol:chloroform:isamyl alcohol and shake vigorously (do not vortex). Centrifuge 5 minutes at maximum speed. Transfer top aqueous solution to a new tube. Ethanol precipitate: add 7.5X 5M NH4OAc and 2.5X volume of 100% ethanol. Centrifuge immediately at room temp. for 20 min, maximum speed. Remove sup then wash pellet 2X with cold 80% ethanol. Remove as much ethanol wash as possible then let pellet air dry. Resuspend pellet in 3ul RNase-free water.

In vitro Transcription (IVT) and labeling with biotin

Pipet 1.5ul of cDNA into a thin-wall PCR tube.

Make NTP labeling mix:

Combine at room temperature: 2ul T7 10xATP (75mM) (Ambion)
2ul T7 10xGTP (75mM) (Ambion)
1.5ul T7 10xCTP (75mM) (Ambion)

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Enzo)

1.5ul T7 10xUTP (75mM) (Ambion)
 3.75ul 10mM Bio-11-UTP (Boehringer-Mannheim/Roche or
 3.75ul 10mM Bio-16-CTP (Enzo)
 2ul 10x T7 transcription buffer (Ambion)
 2ul 10x T7 enzyme mix (Ambion)

Final volume of total reaction is 20ul. Incubate 6 hours at 37C in a PCR machine.

RNeasy clean-up of IVT product

Follow previous instructions for RNeasy columns or refer to Qiagen's RNeasy protocol handbook.

cRNA will most likely need to be ethanol precipitated. Resuspend in a volume compatible with the fragmentation step.

Fragmentation

15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer.

5 x Fragmentation buffer:

200 mM Tris-acetate, pH 8.1
 500 mM KOAc
 150 mM MgOAc

The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range

Hybridization

200 ul (10ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made.

5

Hybridization Mix: fragment labeled RNA (50ng/ul final conc.)

10

50 pM 948-b control oligo

1.5 pM BioB

5 pM BioC

5

25 pM BioD

100 pM CRE

15

0.1mg/ml herring sperm DNA

0.5mg/ml acetylated BSA

to 300 ul with 1xMES hyb. buffer

20

10 The instruction manuals for the products used herein are incorporated herein in their entirety.

Labeling Protocol Provided Herein

Hybridization reaction:

Start with non-biotinylated IVT (purified by RNeasy columns)

25

(see example 1 for steps from tissue to IVT)

15 IVT antisense RNA; 4 µg: µl

Random Hexamers (1 µg/µl): 4 µl

H₂O: µl

30

14 µl

20 - Incubate 70°C, 10 min. Put on ice.

35

Reverse transcription:

5X First Strand (BRL) buffer: 6 µl

0.1 M DTT: 3 µl

50X dNTP mix: 0.6 µl

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25 H₂O: 2.4 µl

Cy3 or Cy5 dUTP (1mM): 3 µl

SS RT II (BRL): 1 µl

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16 µl

30 - Add to hybridization reaction.
- Incubate 30 min., 42°C.
- Add 1 µl SSII and let go for another hour.

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Put on ice.

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- 50X dNTP mix (25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP: 25 µl each of 100mM dATP, dCTP, and dGTP; 10 µl of 100mM dTTP to 15 µl H₂O. dNTPs from Pharmacia)

RNA degradation:

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86 µl H₂O

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- Add 1.5 µl 1M NaOH/ 2mM EDTA, incubate at 65°C, 10 min. 10 µl 10N NaOH

4 µl 50mM EDTA

U-Con 30

500 µl TE/sample spin at 7000g for 10 min, save flow through for purification

20

10

Qiagen purification:

-suspend u-con recovered material in 500µl buffer PB

-proceed w/ normal Qiagen protocol

DNAse digest:

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- Add 1 µl of 1/100 dil of DNAse/30µl Rx and incubate at 37°C for 15 min.

15

-5 min 95°C to denature enzyme

Sample preparation:

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- Add:

Cot-1 DNA: 10 µl

50X dNTPs: 1 µl

20

20X SSC: 2.3 µl

Na pyro phosphate: 7.5 µl

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10mg/ml Herring sperm DNA 1ul of 1/10 dilution

21.8 final vol.

- Dry down in speed vac.

25

- Resuspend in 15 µl H₂O.

40

- Add 0.38 µl 10% SDS.

- Heat 95°C, 2 min.

- Slow cool at room temp. for 20 min.

Put on slide and hybridize overnight at 64°C.

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Washing after the hybridization:

3X SSC/0.03% SDS: 2 min. 37.5 mls 20X SSC+0.75mls 10% SDS in 250mls H₂O

1X SSC: 5 min. 12.5 mls 20X SSC in 250mls H₂O

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0.2X SSC: 5 min. 2.5 mls 20X SSC in 250mls H₂O

Dry slides in centrifuge, 1000 RPM, 1min.

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Scan at appropriate PMT's and channels.

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5 The results are shown in Figures 1 through 11. The lists of genes come from colorectal tumors
from a variety of stages of the disease. The genes that are up regulated in the tumors (overall)
10 were also found to be expressed at a limited amount or not at all in the body map. The body map
for the colorectal project consists of ten tissues: Heart, Brain, Lung, Liver, Breast, Kidney,
Prostate, Small Intestine, Spleen, and Colon. The down regulated genes in tumors (overall)
versus normal colon were not selected for their expression or lack of expression in the body map.
15 As indicated, some of the Accession numbers include expression sequence tags (ESTs). Thus, in
one embodiment herein, genes within an expression profile, also termed expression profile genes,
include ESTs and are not necessarily full length. Figure 1 shows 51 upregulated genes; Figure 2
shows 194 upregulated genes; Figure 3 shows 1144 upregulated genes and Figure 4 shows 1815
upregulated genes. The genes shown in Figures 1 and 5 are particularly preferred. Figure 5
20 shows 54 downregulated genes; Figure 6 shows 558 downregulated genes; and Figure 7 shows
1923 downregulated genes; and Figures 8, 9, 10 and 11 provide the Accession numbers for
genes, including expression sequence tags, upregulated in tumor tissue compared to normal
colon tissue.

Example 2

35

20 Expression studies were performed herein.

40

As indicated in Figure 21, CAA2 is upregulated in colon cancer tissue. CAA2 is found in
chromosome 15, cytoband 15q15-22, interval D15S146-D15S117. CAA2 has N-myristoylation
sites and a C-terminal microbody targeting signal. The preferred fragments shown in Figures 18
and 19 have a solubility of 1 mg/ 1 ml H₂O.

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25 As indicated in Figure 26, CAA9 is upregulated in colon cancer tissue. CAA9 is found in
chromosome 5, cytoband 5q23.3, interval D5S471-D5S393.

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As indicated in Figures 30A and 30B, CGA7 is upregulated in colon cancer tissue. CGA7 is found
in chromosome 2.

As indicated in Figure 34, CGA8 is upregulated in colon cancer tissue.

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As indicated in Figure 37, CJA8 is upregulated in colon cancer tissue. CJA8 is found in chromosome 11.

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As indicated in Figure 38, BCN7 is upregulated in colon cancer tissue. BCN7 is found in chromosome 5, cytoband 5q22, interval D5S471-D5S393.

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Claims

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CLAIMS

We claim:

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1. A method of screening drug candidates comprising:
- a) providing a cell that expresses an expression profile gene which encodes a protein selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7 and CQA2 or a fragment thereof;
- b) adding a drug candidate to said cell; and
- c) determining the effect of said drug candidate on the expression of said expression profile gene.

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2. A method according to claim 1 wherein said determining comprises comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of said drug candidate, wherein the concentration of said drug candidate can vary when present, and wherein said comparison can occur after addition or removal of the drug candidate.

25

3. A method according to claim 1 wherein the expression of said profile gene is decreased as a result of the introduction of the drug candidate.

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4. A method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the binding of said candidate agent to said CCMP.

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5. A method for screening for a bioactive agent capable of modulating the activity of a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the effect of said candidate agent on the bioactivity of said CCMP.

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6. A method of evaluating the effect of a candidate colorectal cancer drug comprising:
- a) administering said drug to a patient;
- b) removing a cell sample from said patient; and
- c) determining the expression profile of said cell.

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7. A method according to claim 6 further comprising comparing said expression profile to an expression profile of a healthy individual.

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8. A biochip comprising a nucleic acid segment encoding CJA81 or a fragment thereof, wherein said biochip comprises fewer than 1000 nucleic acid probes.

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9. A method of diagnosing colorectal cancer comprising:

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a) determining the expression of a gene encoding CJA8 or a fragment thereof in a first tissue type of a first individual; and

15

b) comparing said expression of said gene from a second normal tissue type from said first individual or a second unaffected individual;

wherein a difference in said expression indicates that the first individual has colorectal cancer.

20

10. An antibody which specifically binds to CJA8, or a fragment thereof.

10

11. An antibody which specifically binds to CAA9, or a fragment thereof.

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12. The antibody of Claim 11 wherein said fragment is selected from the group CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.

13. The antibody of Claim 10, wherein said antibody is a monoclonal antibody.

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14. The antibody of Claim 10, wherein said antibody is a humanized antibody.

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15. The antibody of Claim 10, wherein said antibody is an antibody fragment.

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16. A method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer modulator protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof, said method comprising:

20

a) combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody

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which binds to said CCMP or fragment thereof; and

b) determining the binding of said CCMP or fragment thereof and said antibody.

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17. A method for inhibiting colorectal cancer, said method comprising administering to a cell a composition comprising an antibody to CJA8 or a fragment thereof.

18. The method of Claim 17 wherein said cell is a cell of an individual.

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19. The method of Claim 18 wherein said individual has cancer.

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20. The method of Claim 17 wherein said antibody is a humanized antibody.

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21. The method of Claim 17 wherein said antibody is an antibody fragment.

22. A method for inhibiting colorectal cancer in a cell, wherein said method comprises administering to a cell a composition comprising antisense molecules to CJA8.

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5 23. A peptide consisting essentially of CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 or CAA9p5MAPS.

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24. A composition comprising the peptide of Claim 23.

25. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising CJA8 or a fragment thereof.

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10 26. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof.

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27. A composition capable of eliciting an immune response in an individual, said composition comprising CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.

15 28. A composition capable of eliciting an immune response in an individual, said composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.

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29. A method of treating an individual for colorectal cancer comprising administering to said individual an inhibitor of CJA8.

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20 30. The method of Claim 29 wherein said inhibitor is an antibody.

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31. A method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

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32. A method of neutralizing the effect of a CJA8, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization.

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33. A method for localizing a therapeutic moiety to colorectal cancer tissue comprising exposing said tissue to an antibody to CJA8 or fragment thereof conjugated to said therapeutic moiety.

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34. The method of Claim 33, wherein said therapeutic moiety is a cytotoxic agent.

35. The method of Claim 33, wherein said therapeutic moiety is a radioisotope.

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36. A method of treating colorectal cancer comprising administering to an individual having colorectal cancer an antibody to CJA8 or fragment thereof conjugated to a therapeutic moiety.

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37. The method of Claim 36, wherein said therapeutic moiety is a cytotoxic agent.

38. The method of Claim 36, wherein said therapeutic moiety is a radioisotope.

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FIGURE 1

Primary Key	fold upregulated in Tumor over normal colon	Accession	Unigene CLUSTER	Unigene Descriptor	Unigene complete cds
37677	>10	AA460530	Hs.98384	Homo sapiens orphan G protein-coupled receptor HG38	mRNA complete cds
6449	>10	X89986	Hs.32935	H. sapiens mRNA for NBK apoptotic inducer protein	
4178	>10	U30246	Hs.110736	Human burninamide-sensitive Na-K-Cl cotransporter (NKCC1)	mRNA complete cds
18330	>10	AA216722	Hs.54481	Human mRNA for apolipoprotein E receptor 2	complete cds
5692	>10	X17644	Hs.2707	G1 to S phase transition 1	
16910	>10	AA053636	Hs.129849	PBK1	
33109	>10	W59951	Hs.22564	Human mRNA for KIAA0389 gene complete cds	
37246	>10	AA449311	Hs.98658	Homo sapiens mitotic checkpoint protein kinase (BUB1)	mRNA complete cds
2857	>10	M58507	Hs.2173	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)	
14338	>10	AA598712	Hs.23723	ESTs Weakly similar to ORF YPL212c (S cerevisiae)	
4676	9.6	U55206	Hs.78619	Homo sapiens human gamma-glutamyl hydrolase (hGlt)	mRNA complete cds
2192	7.8	L48211	Hs.20954	Homo Sapiens angiotensin II receptor gene complete cds	
5793	7.4	X54942	Hs.83758	CDC28 protein kinase 2	
18231	6.3	AA199747	Hs.79025	Human mRNA for KIAA0096 gene partial cds	
6061	6.1	X68314	Hs.2704	Glutathione peroxidase 2 gastrointestinal	
27117	5.0	AA405098	Hs.38178	ESTs Weakly similar to MOESIN/ELAVIN/HOMOLOG (D melanogaster)	
12059	5.0	AA417030	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1)	mRNA complete cds
1106	4.8	HG2981-HT3127		EST - HG2981-HT3127	
2157	4.6	L41939	Hs.89403	Homo sapiens protein-tyrosine Kinase EPHB2v (EPH2v)	mRNA complete cds
13193	4.4	AA442763	Hs.20483	ESTs Highly similar to G2MITOTIC-SPECIFIC CYCLIN B2 (Mesocricetus auratus)	
5690	4.4	X17620	Hs.118638	NUCLEOSIDE DIPHOSPHATE KINASE A	
28050	4.1	AA479139	Hs.75393	Acid phosphatase 1 soluble	
4540	3.5	U48807	Hs.2359	Human MAP kinase phosphatase (MKP-2)	mRNA complete cds
26105	3.1	AA243133	Hs.48915	Homo sapiens serine/threonine kinase (BTAK)	mRNA complete cds
19177	3.1	H10984	Hs.12338	ESTs	
5780	3.1	X54489	Hs.789	GRO1 oncogene (metanoma growth stimulating activity alpha)	
33620	3.0	W93043	Hs.59509	ESTs	
4536	2.9	U48705	Hs.75562	Receptor protein-tyrosine Kinase EDDR1	
5928	2.9	X62048	Hs.75188	WEE1-LIKE PROTEIN KINASE	
28258	2.8	AA505133	Hs.62273	ESTs	
21266	2.7	R09195	Hs.151385	Homo sapiens mRNA for KIAA0564 protein partial cds	

FIGURE 1 (CONT.)

27746	2.5	AA453159	Hs.41723	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds
28310	2.5	AA048746	Hs.110457	ESTs
2640	2.4	M30448	EST - M30448	
3834	2.3	U12595	Hs.2204	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA partial cds
4674	2.3	U54898	Hs.93121	Human LGN protein mRNA complete cds
5769	2.3	X53800	Hs.89690	GRO3 oncogene
25050	2.3	AA011134	Hs.25663	ESTs Weakly similar to renin [H.sapiens]
41935	2.3	T29681	Hs.75761	Human serine kinase mRNA complete cds
26895	2.3	AA292765	Hs.42650	H.sapiens mRNA for M-phase phosphoprotein mpp5
1782	2.1	L12711	Hs.89643	Transketolase (Wernicke-Korsakoff syndrome)
25593	2.1	AA113149	Hs.8130	Homo sapiens IPL (IPL) mRNA complete cds
1487	1.8	J03934	Hs.80705	NAD(P)H:menadiolone oxidoreductase
7656	1.5	AA203428	Hs.7758	ESTs Moderately similar to ANKYRIN BRAIN VARIANT 2 [Homo sapiens]
683	1.5	D79997	Hs.41697	Human mRNA for KIAA0175 gene complete cds
836	1.5	D87444	Hs.79305	Human mRNA for KIAA0255 gene complete cds
3098	1.2	M77836	Hs.78217	PYRROLINE-5-CARBOXYLATE REDUCTASE
6879	1.1	Z20066	Hs.80896	H.sapiens nek2 mRNA for protein kinase
6880	1.0	Z29067	Hs.2236	H.sapiens nek3 mRNA for protein kinase
2473	0.7	M21904	Hs.79748	Antigen identified by monoclonal antibodies 4F2 TRA1.10 TROP4 and T43
36508	0.7	AA429621	Hs.79093	Human 100 kDa coactivator mRNA complete cds

FIGURE 2

Primary Key	fold upregulated of Tumor	Accession	Unigene CLUSTER	Unigene Descriptor
33616	>10	W93726	Hs.55279	Protease inhibitor 5 (maspin)
34197	>10	AA232315	Hs.12540	Homo sapiens clone 23797 and 23917 mRNA partial cds
19387	>10	H20128	Hs.31656	ESTs
8125	>10	AA330771	Hs.82911	Human protein-tyrosine phosphatase (IU-PP-1) mRNA partial sequence
18362	>10	AA223912	Hs.12013	Ribonuclease L (2'-5'-oligoadenylate synthetase-dependent) inhibitor
39995	>10	H62474	Hs.108240	EST
18328	>10	H17808	Hs.22858	ESTs
39590	>10	AA598648	Hs.78202	Human mRNA for transcriptional activator RSNF2b complete cds
38456	>10	AA504343	Hs.101074	ESTs
17559	>10	AA128407	Hs.71190	ESTs
5519	>10	X14850	Hs.2711	HISTONE H2A.X
4029	>10	U21090	Hs.74598	Human DNA polymerase delta small subunit mRNA complete cds
15008	>10	U30246	Hs.110735	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
3559	>10	U04313	Hs.55279	Protease inhibitor 5 (maspin)
26916	>10	AA331393	Hs.47378	ESTs
1346	>10	HG4716-HT5158	EST - HG4716-HT5158	
37491	10.0	AA455239	Hs.87630	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 (Caenorhabditis elegans)
13110	9.8	AA435840	Hs.19114	Homo sapiens mRNA for high mobility group protein HMG2a
4676	9.8	U55206	Hs.78619	Homo sapiens human gamma-glutamyl hydrolase (NGH) mRNA complete cds
21655	8.7	R38239	Hs.34782	EST
14723	8.3	D59894	Hs.83758	CDC28 protein kinase 2
5793	7.4	X54942	Hs.124215	ESTs
29848	7.1	N22107	Hs.112013	ESTs
9347	7.0	H03686	Hs.112013	ESTs
6078	7.0	X69141	Hs.48876	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE
9326	6.8	D89377	Hs.89404	Msh (Drosophila) homeo box homolog 2
1566	6.7	J05614	EST - J05614	
25875	6.7	AA129757	Hs.54602	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 (Rattus norvegicus)
20126	6.4	N22015	Hs.18457	ESTs
6061	6.1	X68314	Hs.2704	Glutathione peroxidase 2 gastrointestinal
10867	6.1	AA088458	Hs.19322	ESTs Weakly similar to ALU SUBFAMILY J1
18062	6.0	AA178945	Hs.73625	ESTs Moderately similar to rabkinesin-5 (M. musculus)
4003	5.9	U25182	Hs.83383	Human antioxidant enzyme AOE37.2 mRNA complete cds
18290	5.8	AA211001	Hs.86430	ESTs
5330	5.8	U91327	EST - U91327	
4244	5.7	U33286	Hs.90073	Human chromosome segregation gene homolog CAS mRNA complete cds

FIGURE 2 (CONT.)

6928	5.7	Z46629	Hs.2316	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)
6160	5.8	X74794	Hs.89599	CDG21 HOMOLOG
31487	5.4	N69507	Hs.120849	ESTs
9470	5.3	H46617	EST - H46617	
33458	5.0	W66635	Hs.14150	Homo sapiens mRNA for KIA0536 protein complete cds
12669	5.0	AA417030	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
1108	4.8	HC2961-IT3127	EST - HC2961-IT3127	
34367	4.8	AA251758	Hs.40323	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds
11595	4.8	AA242819	Hs.32539	ESTs
17622	4.8	AA131584	Hs.71435	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]
34754	4.7	AA287642	Hs.81848	Human mRNA for KIA0078 gene complete cds
25038	4.7	AA010085	Hs.83758	CDG28 protein kinase 2
5312	4.6	U90716	Hs.78187	Human cell surface protein HCAR mRNA complete cds
8095	4.6	AA314779	Hs.105484	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
33566	4.6	W95477	Hs.50592	ESTs
8264	4.5	AA401334	Hs.106941	ESTs
34479	4.5	AA262080	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
7898	4.4	AA263032	Hs.81634	ESTs
10716	4.4	AA053319	Hs.5951	ESTs
9690	4.4	X17620	Hs.118638	NUCLEOSIDE DIPHOSPHATE KINASE A
20203	4.3	N26855	Hs.5858	ESTs Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]
10923	4.2	AA116036	Hs.9329	ESTs
28050	4.1	AA479139	Hs.75393	Acid phosphatase 1 soluble
10970	4.1	AA126360	Hs.5285	ESTs
4149	4.1	U28386	- Hs.2397	RAG (recombination activating gene) cohort 1
5767	4.1	X53763	Hs.118226	MULTIFUNCTIONAL PROTEIN ADE2
26596	4.0	AA279943	Hs.88671	ESTs
8861	3.8	AFFX-	AFFX-HUNTFRM11507_3	
38504	3.8	AA596803	Hs.111496	ESTs
30560	3.8	N48284	Hs.1334	MYB PROTO-ONCOGENE PROTEIN
8513	3.8	AA446990	Hs.103135	ESTs
14509	3.8	AA609843	Hs.32793	ESTs
25284	3.8	AA045074	Hs.110145	ESTs Weakly similar to 52 kD SS-A/Ro autoantigen [H.sapiens]
27354	3.8	AA425221	Hs.81688	ESTs
18385	3.8	AA227219	Hs.110828	Homo sapiens CAGf9 mRNA partial cds
25240	3.7	AA039713	Hs.110406	ESTs
16654	3.7	AA055552	Hs.71622	ESTs Weakly similar to KIA00319 [H.sapiens]
3709	3.7	U07550	Hs.1197	Heat shock 10 kD protein 1 (chaperonin 10)
13606	3.5	AA456437	Hs.20386	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 kD SUBUNIT [H.sapiens]
8338	3.4	AA417152	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds

FIGURE 2 (CONT.)

387	D28589	EST - D28589	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]
15643	W50247	Hs.27437	ESTs
13838	AA465342	Hs.34045	ESTs
251	D14520	Hs.84728	Basic transcription element binding protein 2
3778	U09848	Hs.363	Zinc finger protein 139 (clone pHz-37)
5600	X16398	Hs.37791	NAD-DEPENDENT METHYLENE TETRAHYDROFOLATE DEHYDROGENASE
17365	AA101551	Hs.68900	ESTs
33985	AA181580	Hs.81690	Homo sapiens importin beta subunit mRNA complete cds
19233	H12534	Hs.8104	ESTs
13767	AA463234	Hs.119387	ESTs
4738	U58766	Hs.75801	Human FX protein mRNA complete cds
17041	AA070364	EST - RC_AA070364	ESTs
15504	W28362	Hs.44131	ESTs
7401	AA094800	Hs.55582	Human translation initiation factor eIF3 p65 subunit mRNA complete cds
18683	F04258	Hs.36454	ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]
23930	I96690	Hs.125123	ESTs Weakly similar to IIII ALU SUBFAMILY
11288	AA196512	Ils.25916	ESTs
170	D00596	Hs.82962	Thymidylate synthase
11659	AA251809	Hs.38708	Homo sapiens MAD3-like protein kinase mRNA complete cds
14134	AA489080	Hs.3568	ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]
11140	AA159132	Hs.11817	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]
17925	AA164209	Hs.31730	Homo sapiens RRM RNA binding protein GRYBP (GRY-RBP) mRNA complete cds
28530	AA278550	Hs.73281	ESTs
7445	AA104023	Hs.110048	ESTs
18055	AA179387	Hs.73596	ESTs
15174	U82987	Hs.87246	Human Bcl-2 binding component 3 (bcl3) mRNA partial cds
33620	V93943	Hs.59509	ESTs
1932	I24804	Hs.75839	Human p23 mRNA complete cds
39556	F03738	Hs.3657	ESTs
1605	L00058	Hs.70070	V-myc avian myelocytomatosis viral oncogene homolog
4536	U48705	Hs.75562	Receptor protein-tyrosine kinase EDDR1
36200	AA421164	Hs.107213	ESTs
12313	AA387516	Hs.22595	ESTs
19867	H61476	Hs.15641	ESTs
6081	X59390	Hs.82685	CD47 antigen (Rb-related antigen integrin-associated signal transducer)
16708	AA043944	Hs.62663	ESTs
357	D28156	Hs.78202	Human mRNA for transcriptional activator hSNF2b complete cds
8059	AA310967	Hs.5080	ESTs Weakly similar to T04A8.11 [C.elegans]
38830	AA411448	Hs.139386	ESTs
20151	N22895	Hs.6831	Homo sapiens clone 1400 unknown protein mRNA partial cds

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FIGURE 2 (CONT.)

28258	2.8	AA505133	Hs.62273	ESTs	ESTs	
8816	2.8	AA460077	Hs.28555	ESTs	ESTs	
6480	2.8	X91788	Hs.84974	H. sapiens mRNA for lcn protein		
14560	2.8	AA621122	Hs.5198	ESTs	ESTs	
35955	2.7	AA412528	Hs.21766	ESTs	ESTs	
17642	2.7	AA132983	Hs.20183	ESTs	ESTs	Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R. norvegicus]
6131	2.7	X72841	Hs.44155	ESTs	ESTs	Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [H. sapiens]
6444	2.7	X69750	Hs.2758	Human retinoblastoma-binding protein (RbAp48) mRNA complete cds		
7701	2.7	AA215333	Hs.90077	H. sapiens mRNA for TGIF protein		
42534	2.7	W73189	Hs.97101	ESTs	ESTs	
34796	2.7	AA291259	Hs.89403	Homo sapiens protein-tyrosine kinase EPHB2 (EPHB2) mRNA complete cds		
1923	2.7	L23808	Hs.97101	ESTs	ESTs	
10951	2.6	AA126719	Hs.1695	Matrix metalloproteinase 12 (macrophage elastase)		
11308	2.6	AA207114	Hs.25282	ESTs	ESTs	
4086	2.6	U24704	Hs.27842	ESTs	ESTs	
5587	2.6	X13482	Hs.111709	Human anilase secretory factor-1 mRNA complete cds		
19841	2.6	H59617	Hs.80506	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'		
7614	2.6	AA187579	Hs.5169	ESTs	ESTs	Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster]
11362	2.6	AA227261	Hs.102696	ESTs	ESTs	Weakly similar to Yel007c-ap [S. cerevisiae]
13866	2.6	AA476319	Hs.20922	ESTs	ESTs	
2993	2.6	M64929	Hs.5327	ESTs	ESTs	
12986	2.6	AA430032	Hs.75200	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform		
5932	2.5	X62153	Hs.7487	ESTs	ESTs	Moderately similar to PTTG gene product [R. norvegicus]
38434	2.5	AA487013	Hs.82479	Minichromosome maintenance deficient (S. cerevisiae) 3		
39185	2.5	AA487508	Hs.142592	ESTs	ESTs	
1424	2.5	J02645	Hs.9877	Homo sapiens mRNA for KIAA0608 protein complete cds		
21876	2.5	R43288	Hs.81613	Eukaryotic translation initiation factor 2A		
6485	2.5	X92098	Hs.75914	EST - RC_R43288		
7960	2.4	AA285277	Hs.6932	H. sapiens mRNA for transmembrane protein mp24		
452	2.4	D38076	Hs.24763	Homo sapiens brain expressed ring finger protein mRNA complete cds		
11701	2.4	AA253031	Hs.31730	RNA binding protein 1		
36380	2.4	AA426291	Hs.108527	Homo sapiens RRM RNA binding protein Gyr-bp (GRY-RBP) mRNA complete cds		
14420	2.4	AA600322	Hs.19574	ESTs	ESTs	Weakly similar to No definition line found [C. elegans]
6387	2.4	X85372	Hs.105465	ESTs	ESTs	Highly similar to AAC-RICH MRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]
1407	2.4	J04088	Hs.3378	H. sapiens mRNA for Sm protein F		
27872	2.4	AA459254	Hs.46855	Topoisomerase (DNA) II alpha (170KD)		
8163	2.4	AA357394	Hs.98073	ESTs	ESTs	
23065	2.4	J23539	Hs.7165	ESTs	ESTs	Highly similar to zinc finger protein [M. musculus]
20637	2.4	N69263	Hs.20524	ESTs	ESTs	Highly similar to HEXOKINASE TYPE I [Homo sapiens]

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FIGURE 2 (CONT.)

17352	2.3	AA100925	Hs.20990	ESTs	EST - RC_D51272_s
28786	2.3	D51272	Hs.4310	ESTs	
26679	2.3	AA281733	Hs.14811	ESTs	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds
24092	2.3	W42845	Hs.83532	ESTs	Membrane cofactor protein (CD46) trophoblast-lymphocyte cross-reactive antigen
5875	2.3	X59405	Hs.7381	ESTs	Homo sapiens voltage dependent anion channel protein mRNA complete cds
7404	2.3	A4094989	Hs.77496	ESTs	H. sapiens mRNA for Sm protein G
6308	2.3	X83373	Hs.25863	ESTs	ESTs Weakly similar to retin [H.sapiens]
25050	2.3	AA011134	Hs.75761	ESTs	Human serine kinase mRNA complete cds
41935	2.3	T29681	Hs.21486	ESTs	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA
3343	2.3	M97936	Hs.80684	ESTs	High-mobility group (nonhistone chromosomal) protein 2
5937	2.2	X52534	Hs.71475	ESTs	
7387	2.2	AA093977	Hs.5683	ESTs	Homo sapiens mRNA for ATP-dependent RNA helicase H46 complete cds
20843	2.2	N69352	Hs.76887	ESTs	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds
28448	2.2	AA621752	Hs.103300	EST - D78129	
651	2.2	D78129	Hs.21214	ESTs	Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds
11888	2.2	AA252672	Hs.10334	ESTs	
11803	2.2	AA257971	Hs.27931	ESTs	MYB PROTO-ONCOGENE PROTEIN
4046	2.2	U22376	Hs.104058	ESTs	ESTs Weakly similar to HYPOHETICAL 27.4 KD PROTEIN IN MET2-CF7 INTERGENIC REGION [Saccharomyces cerevisiae]
20276	2.2	N32919	Hs.104058	ESTs	ESTs Weakly similar to HYPOHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION [Saccharomyces cerevisiae]
34370	2.1	AA251829	Hs.10600	EST - S75256	
14582	2.1	AA621340	EST - HG1112-HT1112		
3461	2.1	S75256	Hs.77899	ESTs	Tropomyosin alpha chain (skeletal muscle)
924	2.1	W66469	Hs.15313	ESTs	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2 [S.cerevisiae]
24348	2.1	AA112053	Hs.78770	ESTs	Isoludra-ORNA synthetase
10898	2.1	D28473	Hs.10724	ESTs	ESTs Weakly similar to unknown [S.cerevisiae]
381	2.1	AA236018	Hs.8130	ESTs	Homo sapiens IPL (IPL) mRNA complete cds
11528	2.1	AA113149	Hs.107213	ESTs	
25593	2.1	AA481403	Hs.83350	ESTs	Human heterochromatin protein HP1-Hs-gamma mRNA complete cds
30040	2.1	U25312	Hs.83378	ESTs	Cytochrome c oxidase subunit VIb
4111	2.1	AC002115	Hs.89866	EST - D28423	Coproporphyrinogen oxidase (coproporphyrin harderoporphyria)
61	2.0	D16611	EST - D28364	ESTs	
9112	2.0	D28423	Hs.42582	ESTs	
380	2.0	D28364	Hs.5950	ESTs	
377	2.0	AA609710	Hs.9564	ESTs	Human clone 121711 defective mariner transposon Hmar2 mRNA sequence
29379	2.0	W72276	Hs.104558	ESTs	
24230	2.0	H85535			
40212	2.0	AA328993			
8118	2.0				

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Gene	Accession	Location	Function
326-16	W03726	Unigen: Pn.25006	Unigen: Pn.25006
326-17	AA033315	Hs 55279	Proteinase inhibitor 5 (proteinase inhibitor 5)
328-17	AA033315	Hs 55279	Proteinase inhibitor 5 (proteinase inhibitor 5)
328-18	U00128	Hs 13145	Home sapiens clone 23397 and 23317 mRNA, partial cds
328-19	U00128	Hs 13145	Home sapiens clone 23397 and 23317 mRNA, partial cds
329-17	AA027912	Hs 55305	ESTs
329-18	AA027912	Hs 55305	ESTs
329-19	AA027912	Hs 55305	ESTs
329-20	AA027912	Hs 55305	ESTs
329-21	AA027912	Hs 55305	ESTs
329-22	AA027912	Hs 55305	ESTs
329-23	AA027912	Hs 55305	ESTs
329-24	AA027912	Hs 55305	ESTs
329-25	AA027912	Hs 55305	ESTs
329-26	AA027912	Hs 55305	ESTs
329-27	AA027912	Hs 55305	ESTs
329-28	AA027912	Hs 55305	ESTs
329-29	AA027912	Hs 55305	ESTs
329-30	AA027912	Hs 55305	ESTs
329-31	AA027912	Hs 55305	ESTs
329-32	AA027912	Hs 55305	ESTs
329-33	AA027912	Hs 55305	ESTs
329-34	AA027912	Hs 55305	ESTs
329-35	AA027912	Hs 55305	ESTs
329-36	AA027912	Hs 55305	ESTs
329-37	AA027912	Hs 55305	ESTs
329-38	AA027912	Hs 55305	ESTs
329-39	AA027912	Hs 55305	ESTs
329-40	AA027912	Hs 55305	ESTs
329-41	AA027912	Hs 55305	ESTs
329-42	AA027912	Hs 55305	ESTs
329-43	AA027912	Hs 55305	ESTs
329-44	AA027912	Hs 55305	ESTs
329-45	AA027912	Hs 55305	ESTs
329-46	AA027912	Hs 55305	ESTs
329-47	AA027912	Hs 55305	ESTs
329-48	AA027912	Hs 55305	ESTs
329-49	AA027912	Hs 55305	ESTs
329-50	AA027912	Hs 55305	ESTs
329-51	AA027912	Hs 55305	ESTs
329-52	AA027912	Hs 55305	ESTs
329-53	AA027912	Hs 55305	ESTs
329-54	AA027912	Hs 55305	ESTs
329-55	AA027912	Hs 55305	ESTs
329-56	AA027912	Hs 55305	ESTs
329-57	AA027912	Hs 55305	ESTs
329-58	AA027912	Hs 55305	ESTs
329-59	AA027912	Hs 55305	ESTs
329-60	AA027912	Hs 55305	ESTs
329-61	AA027912	Hs 55305	ESTs
329-62	AA027912	Hs 55305	ESTs
329-63	AA027912	Hs 55305	ESTs
329-64	AA027912	Hs 55305	ESTs
329-65	AA027912	Hs 55305	ESTs
329-66	AA027912	Hs 55305	ESTs
329-67	AA027912	Hs 55305	ESTs
329-68	AA027912	Hs 55305	ESTs
329-69	AA027912	Hs 55305	ESTs
329-70	AA027912	Hs 55305	ESTs
329-71	AA027912	Hs 55305	ESTs
329-72	AA027912	Hs 55305	ESTs
329-73	AA027912	Hs 55305	ESTs
329-74	AA027912	Hs 55305	ESTs
329-75	AA027912	Hs 55305	ESTs
329-76	AA027912	Hs 55305	ESTs
329-77	AA027912	Hs 55305	ESTs
329-78	AA027912	Hs 55305	ESTs
329-79	AA027912	Hs 55305	ESTs
329-80	AA027912	Hs 55305	ESTs
329-81	AA027912	Hs 55305	ESTs
329-82	AA027912	Hs 55305	ESTs
329-83	AA027912	Hs 55305	ESTs
329-84	AA027912	Hs 55305	ESTs
329-85	AA027912	Hs 55305	ESTs
329-86	AA027912	Hs 55305	ESTs
329-87	AA027912	Hs 55305	ESTs
329-88	AA027912	Hs 55305	ESTs
329-89	AA027912	Hs 55305	ESTs
329-90	AA027912	Hs 55305	ESTs
329-91	AA027912	Hs 55305	ESTs
329-92	AA027912	Hs 55305	ESTs
329-93	AA027912	Hs 55305	ESTs
329-94	AA027912	Hs 55305	ESTs

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[illegible]

FIGURE 3 (CONT.)

23052	18	TG0971	Hs 12513	ESTs	
23053	18	AA45433	Hs 12317	ESTs	
10510	18	AA08104	Hs 27177	ESTs	
25119	18	AA01128	Hs 13319	H sapiens mRNA for protein 2	
21	18	AB00965	Hs 13060	H sapiens ribosome h1 gene	
18797	18	FGH438	Hs 12421	ESTs	
31211	18	AA01198	Hs 12226	Human sapiens protein phosphatase with 5'-untransl. (PPE1.1) mRNA, complete cds	
23054	18	AA01198	Hs 12226	Human sapiens protein phosphatase with 5'-untransl. (PPE1.1) mRNA, complete cds	
42902	18	W06433	Hs 12613	ESTs	
23272	18	RG2321	Hs 20390	EST	
33110	18	AA032709	Hs 20393	ESTs	Weakly similar to HYPOTHETICAL 80.8 KD PROTEIN TOSHC7 IN CHROMOSOME 1 [C. elegans]
181810	18	AA032936	Hs 12949	ESTs	
29643	18	H15540	Hs 42116	ESTs	
36025	18	AA11540	Hs 42116	ESTs	
15008	18	U02015	Hs 10736	Human sapiens mRNA for KIAA0233 protein, partial cds	
23232	18	AA014823	Hs 10349	ESTs	Human sapiens cDNA, novel, identical mRNA, complete cds
34181	18	AA014823	Hs 10349	ESTs	Human sapiens cDNA, novel, identical mRNA, complete cds
40384	18	H33138	Hs 102118	ESTs	
10214	18	AA001207	Hs 50601	ESTs	
31644	18	AA014823	Hs 10349	ESTs	
33064	18	D00822	Hs 10726	ESTs	
30364	18	N34608	Hs 7748	Human sapiens cDNA 73815 mRNA, sequence	
30393	18	AA428333	Hs 98304	ESTs	
20011	18	AA014823	Hs 10349	ESTs	
23055	18	N01134	Hs 8809	ESTs	
338	18	D13645	Hs 2171	Human mRNA for KIAA0233 gene, complete cds	
3073	18	X14873	Hs 13500	T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR	
33509	18	AA410293	Hs 87811	ESTs	
2243	18	U05948	Hs 24884	Human testis secretory protein 18 kDa (HSP18) mRNA, complete cds	
17911	18	AA014823	Hs 10349	ESTs	
33788	18	AA410293	Hs 87811	ESTs	
3163	18	M44424	Hs 1335	Cathepsin E	
22420	18	R04109	Hs 23457	ESTs	
29537	18	N03888	Hs 107147	ESTs	
30027	18	AA030333	Hs 11357	EST	
42913	18	AA014823	Hs 10349	ESTs	
3637	18	X15877	Hs 1721	Human mRNA for adipo-onc1, inhibitory factor	
29351	18	H01134	Hs 14132	ESTs	
29329	18	F02202	Hs 10090	ESTs	
8155	18	X14331	Hs 24318	Human sapiens polyomavirus 2A (P2A)	
3214	18	U05300	Hs 13500	Human T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR	
30400	18	AA014823	Hs 10349	ESTs	
60900	18	H49104	Hs 79108	NUCLEAR FACTOR RBP140	
31818	18	AA189954	Hs 104820	EST	
21891	18	AA234566	Hs 13518	EST	
22272	18	H48408	Hs 29410	ESTs	
21552	18	H01134	Hs 14132	ESTs	
21552	18	H01134	Hs 14132	ESTs	
23131	18	H01134	Hs 14132	ESTs	
31818	18	AA189954	Hs 104820	EST	
37229	18	AA189954	Hs 104820	EST	
28176	18	AA014823	Hs 10349	ESTs	
33066	18	W06433	Hs 12613	ESTs	
21708	18	AA032709	Hs 12949	ESTs	

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[illegible]

FIGURE 3 (CONT.)

[illegible]

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FIGURE 3 (CONT.)

137	AA13702	Hs 09046	EST
138	AA13900	Hs 09023	EST
139	H59432	Hs 25359	EST
140	C82B89	Hs 82322	Human mRNA for KIAA0213 gene complete cds
141	AA14460	Hs 04611	EST
142	AA14468	Hs 05062	EST
143	X81903	Hs 05062	EST
144	AA50928	Hs 50918	EST
145	N32820	Hs 44532	Human mRNA for diaphanin
146	H41720	Hs 41720	EST
147	H45223	Hs 45223	Human mRNA for UGP-GuMuc polypeptide N acetylglucosaminyl transferase
148	X93589	Hs 89027	EST
149	U11582	Hs 72661	Human beta-amyloid precursor A22 mRNA complete cds
150	U31146	Hs 72661	Human beta-amyloid precursor A22 mRNA complete cds
151	AA18860	Hs 141852	EST
152	AA18871	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
153	AA18878	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
154	AA18879	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
155	AA18880	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
156	AA18881	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
157	AA18882	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
158	AA18883	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
159	AA18884	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
160	AA18885	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
161	AA18886	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
162	AA18887	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
163	AA18888	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
164	AA18889	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
165	AA18890	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
166	AA18891	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
167	AA18892	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
168	AA18893	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
169	AA18894	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
170	AA18895	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
171	AA18896	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
172	AA18897	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
173	AA18898	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
174	AA18899	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
175	AA18900	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
176	AA18901	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
177	AA18902	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
178	AA18903	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
179	AA18904	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
180	AA18905	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
181	AA18906	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
182	AA18907	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
183	AA18908	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
184	AA18909	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
185	AA18910	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
186	AA18911	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
187	AA18912	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
188	AA18913	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
189	AA18914	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
190	AA18915	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
191	AA18916	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
192	AA18917	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
193	AA18918	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
194	AA18919	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
195	AA18920	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
196	AA18921	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
197	AA18922	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
198	AA18923	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
199	AA18924	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
200	AA18925	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
201	AA18926	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
202	AA18927	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
203	AA18928	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
204	AA18929	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
205	AA18930	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
206	AA18931	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
207	AA18932	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
208	AA18933	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
209	AA18934	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
210	AA18935	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
211	AA18936	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
212	AA18937	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
213	AA18938	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
214	AA18939	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
215	AA18940	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
216	AA18941	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
217	AA18942	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
218	AA18943	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
219	AA18944	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
220	AA18945	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
221	AA18946	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
222	AA18947	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
223	AA18948	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
224	AA18949	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
225	AA18950	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
226	AA18951	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
227	AA18952	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
228	AA18953	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
229	AA18954	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
230	AA18955	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
231	AA18956	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
232	AA18957	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
233	AA18958	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
234	AA18959	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
235	AA18960	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
236	AA18961	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
237	AA18962	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
238	AA18963	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
239	AA18964	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
240	AA18965	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
241	AA18966	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
242	AA18967	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
243	AA18968	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
244	AA18969	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
245	AA18970	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
246	AA18971	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
247	AA18972	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
248	AA18973	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
249	AA18974	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
250	AA18975	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
251	AA18976	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
252	AA18977	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
253	AA18978	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
254	AA18979	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
255	AA18980	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
256	AA18981	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
257	AA18982	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
258	AA18983	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
259	AA18984	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
260	AA18985	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
261	AA18986	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
262	AA18987	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
263	AA18988	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
264	AA18989	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
265	AA18990	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
266	AA18991	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
267	AA18992	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
268	AA18993	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
269	AA18994	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
270	AA18995	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
271	AA18996	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
272	AA18997	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
273	AA18998	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
274	AA18999	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
275	AA19000	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
276	AA19001	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
277	AA19002	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
278	AA19003	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
279	AA19004	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
280	AA19005	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
281	AA19006	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
282	AA19007	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
283	AA19008	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
284	AA19009	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
285	AA19010	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
286	AA19011	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
287	AA19012	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
288	AA19013	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
289	AA19014	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
290	AA19015	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
291	AA19016	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
292	AA19017	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
293	AA19018	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
294	AA19019	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
295	AA19020	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
296	AA19021	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
297	AA19022	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
298	AA19023	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
299	AA19024	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
300	AA19025	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
301	AA19026	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
302	AA19027	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
303	AA19028	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
304	AA19029	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
305	AA19030	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
306	AA19031	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
307	AA19032	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
308	AA19033	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
309	AA19034	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
310	AA19035	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
311	AA19036	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
312	AA19037	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
313	AA19038	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
314	AA19039	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
315	AA19040	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
316	AA19041	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
317	AA19042	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
318	AA19043	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
319	AA19044	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
320	AA19045	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
321	AA19046	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
322	AA19047	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
323	AA19048	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
324	AA19049	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
325	AA19050	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
326	AA19051	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
327	AA19052	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
328	AA19053	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
329	AA19054	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
330	AA19055	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
331	AA19056	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
332	AA19057	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
333	AA19058	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
334	AA19059	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
335	AA19060	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
336	AA19061	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
337	AA19062	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
338	AA19063	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
339	AA19064	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
340	AA19065	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
341	AA19066	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
342	AA19067	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
343	AA19068	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
344	AA19069	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
345	AA19070	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
346	AA19071	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
347	AA19072	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
348	AA19073	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
349	AA19074	Hs 115541	Human alpha2(I) type I procollagen alpha2(I) chain mRNA complete cds
350	AA19075	Hs 115541	

FIGURE 3 (CONT.)

10	AA359543	Hs 141444	EST1	
11	U08103	Hs 291236	Human sodium mRNA for TRAF5, complete cds	
12	R09437	Hs 2001	THROMBOXANE SYNTHASE	
13	R08178	Hs 20118	ESTs	
14	AA353400	Hs 104026	ESTs	
15	AA4400	Hs 124000	ESTs	
16	AA6738	Hs 124000	ESTs	
17	AA358411	Hs 41313	EST1 highly similar to N18 RIBOSOMAL PROTEIN L38 (Rblu1a ratnucleolus)	
18	U10960	Hs 41313	Human Nucleo-Ar-Ar antigen (NAE3A3) gene complete cds	
19	R13083	Hs 102020	ESTs	
20	U14844	Hs 121336	ESTs	
21	AA358402	Hs 121336	Human RuvB-like interacting protein RuvB-1 mRNA, complete cds	
22	AA358403	Hs 121336	ESTs	
23	H08162	Hs 08162	EST1 - RC_H08162	
24	H08296	Hs 30930	EST	
25	H11035	Hs 30930	EST - RC_AA3076	
26	AA330776	Hs 00438	Human mRNA for RGA3137 gene, complete cds	
27	AA32252	Hs 00438	Human RGA3137 gene, complete cds	
28	AA358375	Hs 13879	Human H08162H1501_3a	
29	AA358376	Hs 13879	Human H08162H1501_3b	
30	AA359110	Hs 81795	Human H08162H1501_3c	
31	H0374132	Hs 81795	Human H08162H1501_3d	
32	R08208	Hs 35333	ESTs	
33	AA417027	Hs 004187	EST	
34	AA358377	Hs 004187	EST	
35	AA358378	Hs 004187	EST	
36	AA358379	Hs 004187	EST	
37	AA358380	Hs 004187	EST	
38	AA358381	Hs 004187	EST	
39	AA358382	Hs 004187	EST	
40	AA358383	Hs 004187	EST	
41	AA358384	Hs 004187	EST	
42	AA358385	Hs 004187	EST	
43	AA358386	Hs 004187	EST	
44	AA358387	Hs 004187	EST	
45	AA358388	Hs 004187	EST	
46	AA358389	Hs 004187	EST	
47	AA358390	Hs 004187	EST	
48	AA358391	Hs 004187	EST	
49	AA358392	Hs 004187	EST	
50	AA358393	Hs 004187	EST	
51	AA358394	Hs 004187	EST	
52	AA358395	Hs 004187	EST	
53	AA358396	Hs 004187	EST	
54	AA358397	Hs 004187	EST	
55	AA358398	Hs 004187	EST	
56	AA358399	Hs 004187	EST	
57	AA358400	Hs 004187	EST	
58	AA358401	Hs 004187	EST	
59	AA358402	Hs 004187	EST	
60	AA358403	Hs 004187	EST	
61	AA358404	Hs 004187	EST	
62	AA358405	Hs 004187	EST	
63	AA358406	Hs 004187	EST	
64	AA358407	Hs 004187	EST	
65	AA358408	Hs 004187	EST	
66	AA358409	Hs 004187	EST	
67	AA358410	Hs 004187	EST	
68	AA358411	Hs 004187	EST	
69	AA358412	Hs 004187	EST	
70	AA358413	Hs 004187	EST	
71	AA358414	Hs 004187	EST	
72	AA358415	Hs 004187	EST	
73	AA358416	Hs 004187	EST	
74	AA358417	Hs 004187	EST	
75	AA358418	Hs 004187	EST	
76	AA358419	Hs 004187	EST	
77	AA358420	Hs 004187	EST	
78	AA358421	Hs 004187	EST	
79	AA358422	Hs 004187	EST	
80	AA358423	Hs 004187	EST	
81	AA358424	Hs 004187	EST	
82	AA358425	Hs 004187	EST	
83	AA358426	Hs 004187	EST	
84	AA358427	Hs 004187	EST	
85	AA358428	Hs 004187	EST	
86	AA358429	Hs 004187	EST	
87	AA358430	Hs 004187	EST	
88	AA358431	Hs 004187	EST	
89	AA358432	Hs 004187	EST	
90	AA358433	Hs 004187	EST	
91	AA358434	Hs 004187	EST	
92				

FIGURE 3 (CONT.)

10	42390	10	75105	EST, Y02554	10	142070	EST, Y02554
11	42391	11	75106	EST, Y02554	11	142071	M sapiens mRNA for pur alpha extended 3' untranslated region.
12	42392	12	75107	EST, Y02554	12	142072	ESTs Weekly similar to F4889 [C. elegans]
13	42393	13	75108	EST, Y02554	13	142073	EST
14	42394	14	75109	EST, Y02554	14	142074	EST
15	42395	15	75110	EST, Y02554	15	142075	EST
16	42396	16	75111	EST, Y02554	16	142076	EST
17	42397	17	75112	EST, Y02554	17	142077	EST
18	42398	18	75113	EST, Y02554	18	142078	EST
19	42399	19	75114	EST, Y02554	19	142079	Human AL4 mRNA complete cds
20	42400	20	75115	EST, Y02554	20	142080	EST
21	42401	21	75116	EST, Y02554	21	142081	EST
22	42402	22	75117	EST, Y02554	22	142082	EST
23	42403	23	75118	EST, Y02554	23	142083	EST
24	42404	24	75119	EST, Y02554	24	142084	EST
25	42405	25	75120	EST, Y02554	25	142085	EST
26	42406	26	75121	EST, Y02554	26	142086	EST
27	42407	27	75122	EST, Y02554	27	142087	EST
28	42408	28	75123	EST, Y02554	28	142088	EST
29	42409	29	75124	EST, Y02554	29	142089	EST
30	42410	30	75125	EST, Y02554	30	142090	EST
31	42411	31	75126	EST, Y02554	31	142091	EST
32	42412	32	75127	EST, Y02554	32	142092	EST
33	42413	33	75128	EST, Y02554	33	142093	EST
34	42414	34	75129	EST, Y02554	34	142094	EST
35	42415	35	75130	EST, Y02554	35	142095	EST
36	42416	36	75131	EST, Y02554	36	142096	EST
37	42417	37	75132	EST, Y02554	37	142097	EST
38	42418	38	75133	EST, Y02554	38	142098	EST
39	42419	39	75134	EST, Y02554	39	142099	EST
40	42420	40	75135	EST, Y02554	40	142100	EST
41	42421	41	75136	EST, Y02554	41	142101	EST
42	42422	42	75137	EST, Y02554	42	142102	EST
43	42423	43	75138	EST, Y02554	43	142103	EST
44	42424	44	75139	EST, Y02554	44	142104	EST
45	42425	45	75140	EST, Y02554	45	142105	EST
46	42426	46	75141	EST, Y02554	46	142106	EST
47	42427	47	75142	EST, Y02554	47	142107	EST
48	42428	48	75143	EST, Y02554	48	142108	EST
49	42429	49	75144	EST, Y02554	49	142109	EST
50	42430	50	75145	EST, Y02554	50	142110	EST
51	42431	51	75146	EST, Y02554	51	142111	EST
52	42432	52	75147	EST, Y02554	52	142112	EST
53	42433	53	75148	EST, Y02554	53	142113	EST
54	42434	54	75149	EST, Y02554	54	142114	EST
55	42435	55	75150	EST, Y02554	55	142115	EST
56	42436	56	75151	EST, Y02554	56	142116	EST
57	42437	57	75152	EST, Y02554	57	142117	EST
58	42438	58	75153	EST, Y02554	58	142118	EST
59	42439	59	75154	EST, Y02554	59	142119	EST
60	42440	60	75155	EST, Y02554	60	142120	EST
61	42441	61	75156	EST, Y02554	61	142121	EST
62	42442	62	75157	EST, Y02554	62	142122	EST
63	42443	63	75158	EST, Y02554	63	142123	EST
64	42444	64	75159	EST, Y02554	64	142124	EST
65	42445	65	75160	EST, Y02554	65	142125	EST
66	42446	66	75161	EST, Y02554	66	142126	EST
67	42447	67	75162	EST, Y02554	67	142127	EST
68	42448	68	75163	EST, Y02554	68	142128	EST
69	42449	69	75164	EST, Y02554	69	142129	EST
70	42450	70	75165	EST, Y02554	70	142130	EST
71	42451	71	75166	EST, Y02554	71	142131	EST
72	42452	72	75167	EST, Y02554	72	142132	EST
73	42453	73	75168	EST, Y02554	73	142133	EST
74	42454	74	75169	EST, Y02554	74	142134	EST
75	42455	75	75170	EST, Y02554	75	142135	EST
76	42456	76	75171	EST, Y02554	76	142136	EST
77	42457	77	75172	EST, Y02554	77	142137	EST
78	42458	78	75173	EST, Y02554	78	142138	EST
79	42459	79	75174	EST, Y02554	79	142139	EST
80	42460	80	75175	EST, Y02554	80	142140	EST
81	42461	81	75176	EST, Y02554	81	142141	EST
82	42462	82	75177	EST, Y02554	82	142142	EST
83	42463	83	75178	EST, Y02554	83	142143	EST
84	42464	84	75179	EST, Y02554	84	142144	EST
85	42465	85	75180	EST, Y02554	85	142145	EST
86	42466	86	75181	EST, Y02554	86	142146	EST
87	42467	87	75182	EST, Y02554	87	142147	EST
88	42468	88	75183	EST, Y02554	88	142148	EST
89	42469	89	75184	EST, Y02554	89	142149	EST
90	42470	90	75185	EST, Y02554	90	142150	EST
91	42471	91	75186	EST, Y02554	91	142151	EST
92	42472	92	75187	EST, Y02554	92	142152	EST
93	42473	93	75188	EST, Y02554	93	142153	EST
94	42474	94	75189	EST, Y02554	94	142154	EST
95	42475	95	75190	EST, Y02554	95	142155	EST
96	42476	96	75191	EST, Y02554	96	142156	EST
97	42477	97	75192	EST, Y02554	97	142157	EST
98	42478	98	75193	EST, Y02554	98	142158	EST
99	42479	99	75194	EST, Y02554	99	142159	EST
100	42480	100	75195	EST, Y02554	100	142160	EST

FIGURE 3 (CONT.)

24490	A4282354	Hs 111395	EST1	
28838	A4398977	Hs 102345	EST1	
7828	A4109440	Hs 5219	EST1	RC_M3344
28839	A4282355	Hs 102346	EST1	
29111	A4282357	Hs 102347	EST1	
21655	R35219	Hs 35219	EST1	
39663	H04768	Hs 109648	EST1	Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT [Dan laurus]
1049	Q3115-UT206	EST1	HQ231041172608	
32300	R77778	Hs 181108	EST1	
32301	A4282358	Hs 181109	EST1	
32302	A4282359	Hs 181110	EST1	
32303	A4282360	Hs 181111	EST1	
32304	A4282361	Hs 181112	EST1	
32305	A4282362	Hs 181113	EST1	
32306	A4282363	Hs 181114	EST1	
32307	A4282364	Hs 181115	EST1	
32308	A4282365	Hs 181116	EST1	
32309	A4282366	Hs 181117	EST1	
32310	A4282367	Hs 181118	EST1	
32311	A4282368	Hs 181119	EST1	
32312	A4282369	Hs 181120	EST1	
32313	A4282370	Hs 181121	EST1	
32314	A4282371	Hs 181122	EST1	
32315	A4282372	Hs 181123	EST1	
32316	A4282373	Hs 181124	EST1	
32317	A4282374	Hs 181125	EST1	
32318	A4282375	Hs 181126	EST1	
32319	A4282376	Hs 181127	EST1	
32320	A4282377	Hs 181128	EST1	
32321	A4282378	Hs 181129	EST1	
32322	A4282379	Hs 181130	EST1	
32323	A4282380	Hs 181131	EST1	
32324	A4282381	Hs 181132	EST1	
32325	A4282382	Hs 181133	EST1	
32326	A4282383	Hs 181134	EST1	
32327	A4282384	Hs 181135	EST1	
32328	A4282385	Hs 181136	EST1	
32329	A4282386	Hs 181137	EST1	
32330	A4282387	Hs 181138	EST1	
32331	A4282388	Hs 181139	EST1	
32332	A4282389	Hs 181140	EST1	
32333	A4282390	Hs 181141	EST1	
32334	A4282391	Hs 181142	EST1	
32335	A4282392	Hs 181143	EST1	
32336	A4282393	Hs 181144	EST1	
32337	A4282394	Hs 181145	EST1	
32338	A4282395	Hs 181146	EST1	
32339	A4282396	Hs 181147	EST1	
32340	A4282397	Hs 181148	EST1	
32341	A4282398	Hs 181149	EST1	
32342	A4282399	Hs 181150	EST1	
32343	A4282400	Hs 181151	EST1	
32344	A4282401	Hs 181152	EST1	
32345	A4282402	Hs 181153	EST1	
32346	A4282403	Hs 181154	EST1	
32347	A4282404	Hs 181155	EST1	
32348	A4282405	Hs 181156	EST1	
32349	A4282406	Hs 181157	EST1	
32350	A4282407	Hs 181158	EST1	
32351	A4282408	Hs 181159	EST1	
32352	A4282409	Hs 181160	EST1	
32353	A4282410	Hs 181161	EST1	
32354	A4282411	Hs 181162	EST1	
32355	A4282412	Hs 181163	EST1	
32356	A4282413	Hs 181164	EST1	
32357	A4282414	Hs 181165	EST1	
32358	A4282415	Hs 181166	EST1	
32359	A4282416	Hs 181167	EST1	
32360	A4282417	Hs 181168	EST1	
32361	A4282418	Hs 181169	EST1	
32362	A4282419	Hs 181170	EST1	
32363	A4282420	Hs 181171	EST1	
32364	A4282421	Hs 181172	EST1	
32365	A4282422	Hs 181173	EST1	
32366	A4282423	Hs 181174	EST1	
32367	A4282424	Hs 181175	EST1	
32368	A4282425	Hs 181176	EST1	
32369	A4282426	Hs 181177	EST1	
32370	A4282427	Hs 181178	EST1	
32371	A4282428	Hs 181179	EST1	
32372	A4282429	Hs 181180	EST1	
32373	A4282430	Hs 181181	EST1	
32374	A4282431	Hs 181182	EST1	
32375	A4282432	Hs 181183	EST1	
32376	A4282433	Hs 181184	EST1	
32377	A4282434	Hs 181185	EST1	
32378	A4282435	Hs 181186	EST1	
32379	A4282436	Hs 181187	EST1	
32380	A4282437	Hs 181188	EST1	
32381	A4282438	Hs 181189	EST1	
32382	A4282439	Hs 181190	EST1	
32383	A4282440	Hs 181191	EST1	
32384	A4282441	Hs 181192	EST1	
32385	A4282442	Hs 181193	EST1	
32386	A4282443	Hs 181194	EST1	
32387	A4282444	Hs 181195	EST1	
32388	A4282445	Hs 181196	EST1	
32389	A4282446	Hs 181197	EST1	
32390	A4282447	Hs 181198	EST1	
32391	A4282448	Hs 181199	EST1	
32392	A4282449	Hs 181200	EST1	
32393	A4282450	Hs 181201	EST1	
32394	A4282451	Hs 181202	EST1	
32395	A4282452	Hs 181203	EST1	
32396	A4282453	Hs 181204	EST1	
32397	A4282454	Hs 181205	EST1	
32398	A4282455	Hs 181206	EST1	
32399	A4282456	Hs 181207	EST1	
32400	A4282457	Hs 181208	EST1	
32401	A4282458	Hs 181209	EST1	
32402	A4282459	Hs 181210	EST1	
32403	A4282460	Hs 181211	EST1	
32404	A4282461	Hs 181212	EST1	
32405	A4282462	Hs 181213	EST1	
32406	A4282463	Hs 181214	EST1	
32407	A4282464	Hs 181215	EST1	
32408	A4282465	Hs 181216	EST1	
32409	A4282466	Hs 181217	EST1	
32410	A4282467	Hs 181218	EST1	
32411	A4282468	Hs 181219	EST1	
32412	A4282469	Hs 181220	EST1	
32413	A4282470	Hs 181221	EST1	
32414	A4282471	Hs 181222	EST1	
32415	A4282472	Hs 181223	EST1	
32416	A4282473	Hs 181224	EST1	
32417	A4282474	Hs 181225	EST1	
32418	A4282475	Hs 181226	EST1	
32419	A4282476	Hs 181227	EST1	
32420	A4282477	Hs 181228	EST1	
32421	A4282478	Hs 181229	EST1	
32422	A4282479	Hs 181230	EST1	
32423	A4282480	Hs 181231	EST1	
32424	A4282481	Hs 181232	EST1	
32425	A4282482	Hs 181233	EST1	
32426	A4282483	Hs 181234	EST1	
32427	A4282484	Hs 181235	EST1	
32428	A4282485	Hs 181236	EST1	
32429	A4282486	Hs 181237	EST1	
32430	A4282487	Hs 181238	EST1	
32431	A4282488	Hs 181239	EST1	
32432	A4282489	Hs 181240	EST1	
32433	A4282490	Hs 181241	EST1	
32434	A4282491	Hs 181242	EST1	
32435	A4282492	Hs 181243	EST1	
32436	A4282493	Hs 181244	EST1	
32437	A4282494	Hs 181245	EST1	
32438	A4282495	Hs 181246	EST1	
32439	A4282496	Hs 181247	EST1	
32440	A4282497	Hs 181248	EST1	
32441	A4282498	Hs 181249	EST1	
32442	A4282499	Hs 181250	EST1	
32443	A4282500	Hs 181251	EST1	
32444	A4282501	Hs 181252	EST1	
32445	A4282502	Hs 181253	EST1	
32446	A4282503	Hs 181254	EST1	
32447	A4282504	Hs 181255	EST1	
32448	A4282505	Hs 181256	EST1	
32449	A4282506	Hs 181257	EST1	
32450	A4282507	Hs 181258	EST1	
32451	A4282508	Hs 181259	EST1	
32452	A4282509	Hs 181260	EST1	
32453	A4282510	Hs 181261	EST1	
32454	A4282511	Hs 181262	EST1	
32455	A4282512	Hs 181263	EST1	
32456	A4282513	Hs 181264	EST1	
32457	A4282514	Hs 181265	EST1	
32458	A4282515	Hs 181266	EST1	
32459	A4282516	Hs 181267	EST1	
32460	A4282517	Hs 181268	EST1	
32461	A4282518	Hs 181269	EST1	
32462	A4282519	Hs 181270	EST1	
32463	A4282520	Hs 181271	EST1	
32464	A4282521	Hs 181272	EST1	
32465	A4282522	Hs 181273	EST1	
32466	A4282523	Hs 181274	EST1	
32467	A4282524	Hs 181275	EST1	
32468	A4282525	Hs 181276	EST1	
32469	A4282526	Hs 181277	EST1	
32470	A4282527	Hs 181278	EST1	
32471	A4282528	Hs 181279	EST1	
32472	A4282529	Hs 181280	EST1	
32473	A4282530	Hs 181281	EST1	
32474	A4282531	Hs 181282	EST1	
32475	A4282532	Hs 181283	EST1	
32476	A4282533	Hs 181284	EST1	
32477	A4282534	Hs 181285	EST1	
32478	A4282535	Hs 181286	EST1	
32479	A4282536	Hs 181287	EST1	
32480	A4282537	Hs 181288	EST1	
32481	A4282538	Hs 181289	EST1	
32482	A4282539	Hs 181290	EST1	
32483	A4282540	Hs 181291	EST1	
32484	A4282541	Hs 181292	EST1	
32485	A4282542	Hs 181293	EST1	
32486	A4282543	Hs 181294	EST1	
32487	A4282544	Hs 181295	EST1	
32488	A4282545	Hs 181296	EST1	
32489	A4282546	Hs 181297	EST1	
32490	A4282547	Hs 181298	EST1	
32491	A4282548	Hs 181299	EST1	
32492	A4282549	Hs 181300	EST1	
32493	A4282550	Hs 181301	EST1	
32494	A4282551	Hs 181302	EST1	
32495	A4282552	Hs 181303	EST1	
32496	A4282553	Hs 181304	EST1	
32497	A4282554	Hs 181305	EST1	
32498	A4282555	Hs 181306	EST1	
32499	A4282556	Hs 181307	EST1	
32500	A4282557	Hs 181308	EST1	
32501	A4282558	Hs 181309	EST1	
32502	A4282559	Hs 181310	EST1	
32503	A4282560	Hs 181311	EST1	
32504	A4282561	Hs 181312	EST1	
32505	A4282562	Hs 181313	EST1	
32506	A4282563	Hs 181314	EST1	
32507	A4282564	Hs 181315	EST1	
32508	A4282565	Hs 181316	EST1	
32509	A4282566	Hs 181317	EST1	
32510	A4282567	Hs 181318	EST1	
32511	A4282568	Hs 181319	EST1	
32512	A4282569	Hs 181320	EST1	
32513	A4282570	Hs 181321	EST1	
32514	A4282571	Hs 181322	EST1	
32515	A4282572	Hs 181323	EST1	
32516	A4282573	Hs 181324	EST1	
32517	A4282574	Hs 181325	EST1	
32518	A4282575	Hs 181326	EST1	
32519	A4282576	Hs 181327	EST1	
32520	A4282577	Hs 181328	EST1	
32521	A4282578	Hs 181329	EST1	
32522	A4282579	Hs 181330	EST1	
32523	A4282580	Hs 181331	EST1	
32524	A4282581	Hs 181332	EST1	
32525	A4282582	Hs 181333	EST1	
32526	A4282583	Hs 1		

FIGURE 3 (CONT.)

[illegible]

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FIGURE 3 (CONT.)

[illegible]

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50	NS0511	Hs-51105	EST	
51	NS0520	Hs-51106	EST	
52	AS01978	Hs-13390	EST	
53	AS01979	Hs-13390	EST	
54	CB0007	Hs-15078	Human mRNA for KIAA0183 gene partial cds	
55	U31162	Hs-15078	Human mRNA for KIAA0183 gene partial cds	
56	U32466/17344	Hs-15078	Human nucleotide sequence AB03173 mRNA complete cds	
57	U32466	Hs-15078	EST - H03536/17344	
58	AA15324	Hs-17403	EST	
59	LA02354	Hs-17403	EST	
60	AA011137	Hs-109270	EST	
61	X18796	Hs-145020	EST	
62	U31812	Hs-145020	EST	
63	U31812	Hs-145020	EST	
64	AA111901	Hs-86430	EST	
65	CB03281	Hs-27553	Human mRNA for KIAA0197 gene partial cds	
66	U31227	Hs-51194	EST	
67	VS02730	Human zinc finger factor 4, isoform 1 (ZF4-1) gene complete cds		
68	U318107	Hs-72323	Human zinc finger factor 4, isoform 1 (ZF4-1) gene complete cds	
69	U318107	Hs-72323	EST - U01227	
70	VS04955	Hs-109932	EST - RC_AA07149	
71	AA04785	Hs-90073	Human chromosome segregation gene, encoding CAS mRNA complete cds	
72	U32326	Hs-55331	EST	
73	U32326	Hs-55331	EST	
74	U32326	Hs-55331	EST	
75	U32326	Hs-55331	EST	
76	U32326	Hs-55331	EST	
77	U32326	Hs-55331	EST	
78	U32326	Hs-55331	EST	
79	U32326	Hs-55331	EST	
80	U32326	Hs-55331	EST	
81	U32326	Hs-55331	EST	
82	U32326	Hs-55331	EST	
83	U32326	Hs-55331	EST	
84	U32326	Hs-55331	EST	
85	U32326	Hs-55331	EST	
86	U32326	Hs-55331	EST	
87	U32326	Hs-55331	EST	
88	U32326	Hs-55331	EST	
89	U32326	Hs-55331	EST	
90	U32326	Hs-55331	EST	
91	U32326	Hs-55331	EST	
92	U32326	Hs-55331	EST	
93	U32326	Hs-55331	EST	
94	U32326	Hs-55331	EST	
95	U32326	Hs-55331	EST	
96	U32326	Hs-55331	EST	
97	U32326	Hs-55331	EST	
98	U32326	Hs-55331	EST	
99	U32326	Hs-55331	EST	
100	U32326	Hs-55331	EST	

FIGURE 3 (CONT.)

30015	30015	Ms 47076	EST1	Ms 47076	EST1
30113	30113	Ms 47086	EST1	Ms 47086	EST1
30321	30321	Ms 47172	EST1	Ms 47172	EST1
30324	30324	Ms 47331	EST1	Ms 47331	EST1
3094	3094	Ms 47331	EST1	Ms 47331	EST1
1109	1109	Ms 47331	EST1	Ms 47331	EST1
1122	1122	Ms 47331	EST1	Ms 47331	EST1
2406	2406	Ms 47331	EST1	Ms 47331	EST1
2643	2643	Ms 47331	EST1	Ms 47331	EST1
4031	4031	Ms 47331	EST1	Ms 47331	EST1
803	803	Ms 47331	EST1	Ms 47331	EST1
2033	2033	Ms 47331	EST1	Ms 47331	EST1
24129	24129	Ms 47331	EST1	Ms 47331	EST1
26403	26403	Ms 47331	EST1	Ms 47331	EST1
17053	17053	Ms 47331	EST1	Ms 47331	EST1
21506	21506	Ms 47331	EST1	Ms 47331	EST1
35289	35289	Ms 47331	EST1	Ms 47331	EST1
30710	30710	Ms 47331	EST1	Ms 47331	EST1
31903	31903	Ms 47331	EST1	Ms 47331	EST1
25809	25809	Ms 47331	EST1	Ms 47331	EST1
2331	2331	Ms 47331	EST1	Ms 47331	EST1
30792	30792	Ms 47331	EST1	Ms 47331	EST1
41792	41792	Ms 47331	EST1	Ms 47331	EST1
20620	20620	Ms 47331	EST1	Ms 47331	EST1
38900	38900	Ms 47331	EST1	Ms 47331	EST1
47193	47193	Ms 47331	EST1	Ms 47331	EST1
18743	18743	Ms 47331	EST1	Ms 47331	EST1
33743	33743	Ms 47331	EST1	Ms 47331	EST1
33256	33256	Ms 47331	EST1	Ms 47331	EST1
20620	20620	Ms 47331	EST1	Ms 47331	EST1
27095	27095	Ms 47331	EST1	Ms 47331	EST1
16790	16790	Ms 47331	EST1	Ms 47331	EST1
27117	27117	Ms 47331	EST1	Ms 47331	EST1
4304	4304	Ms 47331	EST1	Ms 47331	EST1
34058	34058	Ms 47331	EST1	Ms 47331	EST1
10609	10609	Ms 47331	EST1	Ms 47331	EST1
29701	29701	Ms 47331	EST1	Ms 47331	EST1
20480	20480	Ms 47331	EST1	Ms 47331	EST1
8720	8720	Ms 47331	EST1	Ms 47331	EST1
24024	24024	Ms 47331	EST1	Ms 47331	EST1
18115	18115	Ms 47331	EST1	Ms 47331	EST1
42508	42508	Ms 47331	EST1	Ms 47331	EST1
24761	24761	Ms 47331	EST1	Ms 47331	EST1
11870	11870	Ms 47331	EST1	Ms 47331	EST1
23211	23211	Ms 47331	EST1	Ms 47331	EST1
42611	42611	Ms 47331	EST1	Ms 47331	EST1
38613	38613	Ms 47331	EST1	Ms 47331	EST1
17351	17351	Ms 47331	EST1	Ms 47331	EST1
27238	27238	Ms 47331	EST1	Ms 47331	EST1
18072	18072	Ms 47331	EST1	Ms 47331	EST1
30709	30709	Ms 47331	EST1	Ms 47331	EST1
21433	21433	Ms 47331	EST1	Ms 47331	EST1
30331	30331	Ms 47331	EST1	Ms 47331	EST1
30795	30795	Ms 47331	EST1	Ms 47331	EST1

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FIGURE 3 (CONT.)

2467	46	238108	Hs 27295	EST	
2468	47	Hs 27296	Hs 27296	EST	
1105	48	G193-141.67	EST - HQJ155-AT 427		
1106	49	G7981-113.127	EST - HQ281-HT 3127		
18212	48	AA196508	Hs 80276	ESTs	
34367	48	AA331738	Hs 40233	Homo sapiens spleen ribonucleoprotein BUB3 (BUB3) mRNA, complete cds	
34802	48	AA291468	Hs 86104	ESTs	
3212	48	AA219344	Hs 12959	ESTs	
1189	48	AA219344	Hs 12959	ESTs	
325	48	AA405282	Hs 125014	ESTs	
17822	48	AA113194	Hs 71435	ESTs	Weakly similar to SDF 1 PROTEIN (Sarcophaga cerevisiae)
32791	48	AA400335	Hs 81587	ESTs	
34794	48	AA327842	Hs 81845	Human mRNA for YK0A007's gene, complete cds	
22327	47	T42791	Hs 86110	EST	
1189	47	AA405282	Hs 125014	ESTs	Highly similar to BUB RIBONUCLEOPROTEIN L2 (BubA conserved)
11599	47	AA329687	Hs 12078	ESTs	
34612	47	AA329687	Hs 111882	ESTs	
1137	47	U79796	Hs 74842	Chrysothamnus 5-acyltransferase (E2 component of pyruvate dehydrogenase complex)	
29238	47	AA310205	Hs 83153	CDCC20 protein, clone 2	
19258	47	H16287	Hs 21333	ESTs	
3210	47	Hs 11615	Hs 11615	Human type 1 alpha 2	
3210	47	MA4505	Hs 84489	SOX101 CHANTEL PROTEIN, BRAIN II ALPHA SUBUNIT	
9998	47	L37961	Hs 89545	Integral transmembrane protein 1	
35400	47	AA339253	Hs 87681	Homo sapiens putative DNA methyltransferase (DNMT2) mRNA, complete cds	
32439	47	AA428270	Hs 91817	EST	Weakly similar to HSP90 protein (H. musculus)
32439	47	AA428270	Hs 91817	ESTs	
31881	47	Hs 11615	Hs 11615	Human type 1 alpha 2	
28775	47	AA325778	Hs 93251	ESTs	Highly similar to PRC mRNA SPLICING FACTOR RNA POLYMERASE PHF218 (Saccharomyces cerevisiae)
34326	47	AA425151	Hs 78210	EST - AC_AA113158	
11709	47	AA113136	Hs 84148	Human mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA, complete cds	
1099	47	L397156	Hs 85557	ESTs	
32946	46	AA418847	Hs 125018	ESTs	Human mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA, complete cds
10773	46	AA472950	Hs 252305	ESTs	Weakly similar to LRR6-1 REVERSE TRANSCRIPTASE HOMOLOGY PHYSICUS (conserved)
40415	46	H21814	Hs 100338	Homo sapiens basic helix-loop helix transcription factor MADS (MADS3) mRNA, complete cds	
14174	46	AA088427	Hs 24104	ESTs	Modestly similar to H24104 SUBFAMILY 5C WARNING ENTRY (H. sapiens)
32113	46	AA488540	Hs 111300	ESTs	Modestly similar to p150 (H. sapiens)
3117	46	L295718	Hs 79167	Human cell surface protein HSP60 mRNA, complete cds	
32113	46	AA488540	Hs 111300	ESTs	
32583	46	AA471250	Hs 87343	EST	
29729	46	H99826	Hs 47110	EST	
7803	46	AA052069	Hs 69402	Homo sapiens protein-tyrosine kinase EPHB2 (EPHB2) mRNA, complete cds	
2137	46	L41829	Hs 32054	ESTs	Weakly similar to L41829-1 BETA PRECURSOR (H. sapiens)
32080	46	H11816	Hs 32054	ESTs	Weakly similar to L41829-1 BETA PRECURSOR (H. sapiens)
32080	46	AA471250	Hs 87343	EST	Human cell surface protein HSP60 mRNA, complete cds
321	46	G73233	Hs 17865	Human mRNA for p150 (H. sapiens)	
34600	46	AA182871	Hs 62681	DNA polymerase gamma	
34605	46	W958477	Hs 52532	ESTs	
34605	46	AA182517	Hs 111100	ESTs	Weakly similar to H111100-1 SUBFAMILY 5C WARNING ENTRY (H. sapiens)
9078	46	AA05020	Hs 20011	Adrenocortical synthase	
40282	45	Hs 11615	Hs 11615	Human type 1 alpha 2	
22847	45	Hs 11615	Hs 11615	Human type 1 alpha 2	
41009	45	Hs 11615	Hs 11615	Human type 1 alpha 2	
8794	45	AA401354	Hs 81127	H. sapiens mRNA for Hs 81127 protein	
27828	45	AA431867	Hs 41181	ESTs	
32182	45	AA431867	Hs 41181	ESTs	
15811	45	Hs 5082	Hs 5082	Homo sapiens mRNA for nucleolar protein hNp208	

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FIGURE 3 (CONT.)

[illegible]

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FIGURE 3 (CONT.)

41	D31145	Hs 61332	Phosphogluconic 2-lyase (cytosolic) protein
42	A4218406	Hs 19347	EST1
43	H08191	Hs 865497	EST1
44	H05628	Hs 39704	EST1
45	H05709	Hs 39704	EST1
46	H05778	Hs 133231	EST1
47	A4218095	Hs 108843	H6C.71
48	U78247	Hs 90796	Human clone 23509 mRNA, sequence
49	A384270	Hs 86553	EST1
50	A4218095	Hs 86553	EST1
51	A4218095	Hs 86553	EST1
52	A4218095	Hs 86553	EST1
53	A4218095	Hs 86553	EST1
54	A4218095	Hs 86553	EST1
55	A4218095	Hs 86553	EST1
56	A4218095	Hs 86553	EST1
57	A4218095	Hs 86553	EST1
58	A4218095	Hs 86553	EST1
59	A4218095	Hs 86553	EST1
60	A4218095	Hs 86553	EST1
61	A4218095	Hs 86553	EST1
62	A4218095	Hs 86553	EST1
63	A4218095	Hs 86553	EST1
64	A4218095	Hs 86553	EST1
65	A4218095	Hs 86553	EST1
66	A4218095	Hs 86553	EST1
67	A4218095	Hs 86553	EST1
68	A4218095	Hs 86553	EST1
69	A4218095	Hs 86553	EST1
70	A4218095	Hs 86553	EST1
71	A4218095	Hs 86553	EST1
72	A4218095	Hs 86553	EST1
73	A4218095	Hs 86553	EST1
74	A4218095	Hs 86553	EST1
75	A4218095	Hs 86553	EST1
76	A4218095	Hs 86553	EST1
77	A4218095	Hs 86553	EST1
78	A4218095	Hs 86553	EST1
79	A4218095	Hs 86553	EST1
80	A4218095	Hs 86553	EST1
81	A4218095	Hs 86553	EST1
82	A4218095	Hs 86553	EST1
83	A4218095	Hs 86553	EST1
84	A4218095	Hs 86553	EST1
85	A4218095	Hs 86553	EST1
86	A4218095	Hs 86553	EST1
87	A4218095	Hs 86553	EST1
88	A4218095	Hs 86553	EST1
89	A4218095	Hs 86553	EST1
90	A4218095	Hs 86553	EST1
91	A4218095	Hs 86553	EST1
92	A4218095	Hs 86553	EST1
93	A4218095	Hs 86553	EST1
94	A4218095	Hs 86553	EST1
95	A4218095	Hs 86553	EST1
96	A4218095	Hs 86553	EST1
97	A4218095	Hs 86553	EST1
98	A4218095	Hs 86553	EST1
99	A4218095	Hs 86553	EST1
100	A4218095	Hs 86553	EST1

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FIGURE 3 (CONT.)

[illegible]

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FIGURE 3 (CONT.)

13018	AA183302	Hs 34053	EST1a	
24515	AA117389	Hs 107830	MAO1 (CS110)	
34016	AA191489	Hs 72614	Human high-affinity copper uptake protein (HCTR1) mRNA, complete cds	
351	D14320	Hs 81178	Basic transcription element binding protein 2	
3778	U09844	Hs 363	Zinc finger protein 139 (clone pZ1.37)	
3845	U09844	Hs 363	Zinc finger protein 139 (clone pZ1.37)	
1448	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
19177	AA100698	Hs 33641	EST1a	
36883	AA132288	Hs 124910	EST1a	
28149	AA250814	Hs 80478	EST1a	Weakly similar to ZINC FINGER PROTEIN 91 (H sapiens)
4011	U20338	Hs 3780	Human cysteine protease Mch2 homolog alpha (MCH2) mRNA, complete cds	
41001	H72584	Hs 3748	EST1a	
13020	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
18256	H11829	Hs 21390	EST1a	
42323	T88152	Hs 79432	Fibrin-2	
33678	AA242360	Hs 47337	EST1a	
22417	H52563	Hs 26593	EST1a	
18278	H17453	Hs 13259	EST1a	
3247	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
17853	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
15296	W18884	Hs 7284	EST1a	Nucleic acid sequence is similar to S. cerevisiae hypoxanthine phosphoribosyl transferase (HYP) (H sapiens)
17873	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
40332	H97365	Hs 108509	Home region mRNA from chromosome 5q21.2, clone A2A	
1719	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
3187	H61185	Hs 43125	Home region mRNA for KIAA1178, gene, partial cds	
33895	AA181580	Hs 81830	Home region mRNA for KIAA1178, gene, partial cds	
5370	H61185	Hs 24837	Home region mRNA for KIAA1178, gene, partial cds	
37251	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
846	D58813	Hs 78348	Home region mRNA for KIAA1178, gene, partial cds	
21807	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
42194	W62318	Hs 82332	EST1a	Most likely similar to anion-specific protein (H sapiens)
18233	AA250814	Hs 8729	EST1a	Most likely similar to anion-specific protein (H sapiens)
42183	H13234	Hs 81204	EST1a	
12829	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
21807	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
13167	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
4728	U58788	Hs 73801	Human TX protein mRNA, complete cds	
7235	AA073427	Hs 17398	EST1a	
17041	AA073427	Hs 17398	EST1a	
15504	W62318	Hs 82332	EST1a	
18714	AA186535	Hs 82081	EST1a	
7401	AA186535	Hs 82081	EST1a	
18712	F10113	Hs 15475	Home region mRNA for KIAA1178, gene, partial cds	
26317	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
9410	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
18683	F01258	Hs 36454	EST1a	Highly similar to HORGANIC PHOSPHATASE (H sapiens)
33891	HUNTFRM11387	AA132718	Human mRNA for KIAA1178, gene, partial cds	
14435	AA057320	Hs 4192	EST1a	Weakly similar to ELONGATION FACTOR 1A1 (H sapiens)
9184	H81128	Hs 41127	EST1a	Weakly similar to ELONGATION FACTOR 1A1 (H sapiens)
22081	H81128	Hs 41127	EST1a	Weakly similar to ELONGATION FACTOR 1A1 (H sapiens)
41823	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
31400	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
15188	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	
15840	AA132718	Hs 80948	Human mRNA for KIAA1178, gene, partial cds	

FIGURE 3 (CONT.)

18250	163509	Hs 24639	EST1	
18251	AA27860	Hs 23291	EST1	
18252	AA25259	Hs 21931	Homo sapiens mRNA for KIAA0248 protein partial cds	
18253	F13700	Hs 115523	Homo sapiens ribonuclease P protein subunit p40 (RPP40) gene complete cds	
18254	U0972	Hs 4287	EST1	
18255	U0973	Hs 4288	EST1	
18256	D13637	Hs 44031	Homo sapiens mRNA for KIAA0202 gene complete cds	
18257	U0948	Hs 14574	Homo sapiens Cdk2 dependent activator protein B1 secretion mRNA complete cds	
18258	AA104023	Hs 110245	EST1	
18259	N65670	Hs 103863	EST1	
18260	AA179387	Hs 73396	EST1	
18261	AA28328	Hs 129391	EST1	
18262	U0949	Hs 103863	EST1	
18263	D37009	Hs 43341	Homo sapiens mRNA for KIAA0202 gene complete cds	
18264	AA504235	Hs 54404	Homo sapiens DNA for immunoglobulin light chain	
18265	R48527	Hs 107450	EST1	
18266	L19161	Hs 121541	TRANSCRIPTIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	
18267	AA283623	Hs 88096	EST1	
18268	AA45648	Hs 103863	EST1	
18269	U0950	Hs 81400	2nd finger protein B1 (p4F2)	
18270	U0951	Hs 87246	Homo sapiens Bcl-2 binding component 3 (Bcl3) mRNA partial cds	
18271	W93943	Hs 95509	EST1	
18272	Y11681	Hs 9364	Homo sapiens ribosomal protein S12 gene nuclear gene encoding nucleolar protein complete cds	
18273	N45028	Hs 125031	EST1	
18274	L24034	Hs 73053	EST1	
18275	U0952	Hs 103863	EST1	
18276	U0953	Hs 89938	EST1	
18277	AA202248	Hs 42882	EST1	
18278	R48281	Hs 142852	EST1	
18279	AA456548	Hs 88096	EST1	
18280	AA281231	Hs 35096	EST1	
18281	AA281231	Hs 35096	EST1	
18282	AA281231	Hs 35096	EST1	
18283	AA281231	Hs 35096	EST1	
18284	AA281231	Hs 35096	EST1	
18285	AA281231	Hs 35096	EST1	
18286	AA281231	Hs 35096	EST1	
18287	AA281231	Hs 35096	EST1	
18288	AA281231	Hs 35096	EST1	
18289	AA281231	Hs 35096	EST1	
18290	AA281231	Hs 35096	EST1	
18291	AA281231	Hs 35096	EST1	
18292	AA281231	Hs 35096	EST1	
18293	AA281231	Hs 35096	EST1	
18294	AA281231	Hs 35096	EST1	
18295	AA281231	Hs 35096	EST1	
18296	AA281231	Hs 35096	EST1	
18297	AA281231	Hs 35096	EST1	
18298	AA281231	Hs 35096	EST1	
18299	AA281231	Hs 35096	EST1	
18300	AA281231	Hs 35096	EST1	
18301	AA281231	Hs 35096	EST1	
18302	AA281231	Hs 35096	EST1	
18303	AA281231	Hs 35096	EST1	
18304	AA281231	Hs 35096	EST1	
18305	AA281231	Hs 35096	EST1	
18306	AA281231	Hs 35096	EST1	
18307	AA281231	Hs 35096	EST1	
18308	AA281231	Hs 35096	EST1	
18309	AA281231	Hs 35096	EST1	
18310	AA281231	Hs 35096	EST1	
18311	AA281231	Hs 35096	EST1	
18312	AA281231	Hs 35096	EST1	
18313	AA281231	Hs 35096	EST1	
18314	AA281231	Hs 35096	EST1	
18315	AA281231	Hs 35096	EST1	
18316	AA281231	Hs 35096	EST1	
18317	AA281231	Hs 35096	EST1	
18318	AA281231	Hs 35096	EST1	
18319	AA281231	Hs 35096	EST1	
18320	AA281231	Hs 35096	EST1	
18321	AA281231	Hs 35096	EST1	
18322	AA281231	Hs 35096	EST1	
18323	AA281231	Hs 35096	EST1	
18324	AA281231	Hs 35096	EST1	
18325	AA281231	Hs 35096	EST1	
18326	AA281231	Hs 35096	EST1	
18327	AA281231	Hs 35096	EST1	
18328	AA281231	Hs 35096	EST1	
18329	AA281231	Hs 35096	EST1	
18330	AA281231	Hs 35096	EST1	
18331	AA281231	Hs 35096	EST1	
18332	AA281231	Hs 35096	EST1	
18333	AA281231	Hs 35096	EST1	
18334	AA281231	Hs 35096	EST1	
18335	AA281231	Hs 35096	EST1	
18336	AA281231	Hs 35096	EST1	
18337	AA281231	Hs 35096	EST1	
18338	AA281231	Hs 35096	EST1	
18339	AA281231	Hs 35096	EST1	
18340	AA281231	Hs 35096	EST1	
18341	AA281231	Hs 35096	EST1	
18342	AA281231	Hs 35096	EST1	
18343	AA281231	Hs 35096	EST1	
18344	AA281231	Hs 35096	EST1	
18345	AA281231	Hs 35096	EST1	
18346	AA281231	Hs 35096	EST1	
18347	AA281231	Hs 35096	EST1	
18348	AA281231	Hs 35096	EST1	
18349	AA281231	Hs 35096	EST1	
18350	AA281231	Hs 35096	EST1	
18351	AA281231	Hs 35096	EST1	
18352	AA281231	Hs 35096	EST1	
18353	AA281231	Hs 35096	EST1	
18354	AA281231	Hs 35096	EST1	
18355	AA281231	Hs 35096	EST1	
18356	AA281231	Hs 35096	EST1	
18357	AA281231	Hs 35096	EST1	
18358	AA281231	Hs 35096	EST1	
18359	AA281231	Hs 35096	EST1	
18360	AA281231	Hs 35096	EST1	
18361	AA281231	Hs 35096	EST1	
18362	AA281231	Hs 35096	EST1	
18363	AA281231	Hs 35096	EST1	
18364	AA281231	Hs 35096	EST1	
18365	AA281231	Hs 35096	EST1	
18366	AA281231	Hs 35096	EST1	
18367	AA281231	Hs 35096	EST1	
18368	AA281231	Hs 35096	EST1	
18369	AA281231	Hs 35096	EST1	
18370	AA281231	Hs 35096	EST1	
18371	AA281231	Hs 35096	EST1	
18372	AA281231	Hs 35096	EST1	
18373	AA281231	Hs 35096	EST1	
18374	AA281231	Hs 35096	EST1	
18375	AA281231	Hs 35096	EST1	
18376	AA281231	Hs 35096	EST1	
18377	AA281231	Hs 35096	EST1	
18378	AA281231	Hs 35096	EST1	
18379	AA281231	Hs 35096	EST1	
18380	AA281231	Hs 35096	EST1	
18381	AA281231	Hs 35096	EST1	
18382	AA281231	Hs 35096	EST1	
18383	AA281231	Hs 35096	EST1	
18384	AA281231	Hs 35096	EST1	
18385	AA281231	Hs 35096	EST1	
18386	AA281231	Hs 35096	EST1	
18387	AA281231	Hs 35096	EST1	
18388	AA281231	Hs 35096	EST1	
18389	AA281231	Hs 35096	EST1	
18390	AA281231	Hs 35096	EST1	
18391	AA281231	Hs 35096	EST1	
18392	AA281231	Hs 35096	EST1	
18393	AA281231	Hs 35096	EST1	
18394	AA281231	Hs 35096	EST1	
18395	AA281231	Hs 35096	EST1	
18396	AA281231	Hs 35096	EST1	
18397	AA281231	Hs 35096	EST1	
18398	AA281231	Hs 35096	EST1	
18399	AA281231	Hs 35096	EST1	
18400	AA281231	Hs 35096	EST1	

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FIGURE 3 (CONT.)

25	A012790	EST	Hs 39072	EST
26	A012790	EST	Hs 39072	EST
27	A012790	EST	Hs 39072	EST
28	A012790	EST	Hs 39072	EST
29	A012790	EST	Hs 39072	EST
30	A012790	EST	Hs 39072	EST
31	A012790	EST	Hs 39072	EST
32	A012790	EST	Hs 39072	EST
33	A012790	EST	Hs 39072	EST
34	A012790	EST	Hs 39072	EST
35	A012790	EST	Hs 39072	EST
36	A012790	EST	Hs 39072	EST
37	A012790	EST	Hs 39072	EST
38	A012790	EST	Hs 39072	EST
39	A012790	EST	Hs 39072	EST
40	A012790	EST	Hs 39072	EST
41	A012790	EST	Hs 39072	EST
42	A012790	EST	Hs 39072	EST
43	A012790	EST	Hs 39072	EST
44	A012790	EST	Hs 39072	EST
45	A012790	EST	Hs 39072	EST
46	A012790	EST	Hs 39072	EST
47	A012790	EST	Hs 39072	EST
48	A012790	EST	Hs 39072	EST
49	A012790	EST	Hs 39072	EST
50	A012790	EST	Hs 39072	EST
51	A012790	EST	Hs 39072	EST
52	A012790	EST	Hs 39072	EST
53	A012790	EST	Hs 39072	EST
54	A012790	EST	Hs 39072	EST
55	A012790	EST	Hs 39072	EST
56	A012790	EST	Hs 39072	EST
57	A012790	EST	Hs 39072	EST
58	A012790	EST	Hs 39072	EST
59	A012790	EST	Hs 39072	EST
60	A012790	EST	Hs 39072	EST
61	A012790	EST	Hs 39072	EST
62	A012790	EST	Hs 39072	EST
63	A012790	EST	Hs 39072	EST
64	A012790	EST	Hs 39072	EST
65	A012790	EST	Hs 39072	EST
66	A012790	EST	Hs 39072	EST
67	A012790	EST	Hs 39072	EST
68	A012790	EST	Hs 39072	EST
69	A012790	EST	Hs 39072	EST
70	A012790	EST	Hs 39072	EST
71	A012790	EST	Hs 39072	EST
72	A012790	EST	Hs 39072	EST
73	A012790	EST	Hs 39072	EST
74	A012790	EST	Hs 39072	EST
75	A012790	EST	Hs 39072	EST
76	A012790	EST	Hs 39072	EST
77	A012790	EST	Hs 39072	EST
78	A012790	EST	Hs 39072	EST
79	A012790	EST	Hs 39072	EST
80	A012790	EST	Hs 39072	EST
81	A012790	EST	Hs 39072	EST
82	A012790	EST	Hs 39072	EST
83	A012790	EST	Hs 39072	EST
84	A012790	EST	Hs 39072	EST
85	A012790	EST	Hs 39072	EST
86	A012790	EST	Hs 39072	EST
87	A012790	EST	Hs 39072	EST
88	A012790	EST	Hs 39072	EST
89	A012790	EST	Hs 39072	EST
90	A012790	EST	Hs 39072	EST
91	A012790	EST	Hs 39072	EST
92	A012790	EST	Hs 39072	EST
93	A012790	EST	Hs 39072	EST
94	A012790	EST	Hs 39072	EST
95	A012790	EST	Hs 39072	EST
96	A012790	EST	Hs 39072	EST
97	A012790	EST	Hs 39072	EST
98	A012790	EST	Hs 39072	EST
99	A012790	EST	Hs 39072	EST
100	A012790	EST	Hs 39072	EST

FIGURE 3 (CONT.)

17642	27	AA132883	Hs 41155	EST, Moderately similar to C-1: TETRAHYDROGLUTE SYNTHASE CYTOSOLIC (H sapiens)
6131	27	X72841	Hs 2756	Human retinoblastoma binding protein (RbAp80) mRNA complete cds
61428	27	R44984	Hs 128182	ESTs
17622	27	AA070815	Hs 121190	EST - RC_AAO70815
2767	27	AA070820	Hs 121190	ESTs
22037	27	U10060	Hs 611	Human c-myc 3' UTR-associated protein 1 (HAP1.3) mRNA complete cds
5163	27	U01120	Hs 118910	Human tumor autoantibody protein (TSA0101) mRNA complete cds
23637	27	H64418	Hs 47820	ESTs
19743	27	AA010300	Hs 60356	ESTs
19594	27	H81020	Hs 33977	ESTs
516	27	H07020	Hs 36017	Human protein tyrosine phosphatase (PTP) mRNA complete cds
5916	27	X28257	Hs 25056	Human mRNA for mutation
42118	27	189724	EST - RC_189724	
7701	27	AA015533	Hs 87101	ESTs
17568	27	AA138905	Hs 22350	ESTs
42314	27	W73189	Hs 69402	Human aspartate aminotransferase (EPR2) mRNA complete cds
23638	27	AA004156	Hs 82825	ESTs
10218	27	R62880	Hs 107823	EST, Moderately similar to C-1: TETRAHYDROGLUTE SYNTHASE CYTOSOLIC (H sapiens)
14789	27	S54641	Hs 73103	H2C-16
32991	27	W03506	Hs 77183	Human mRNA for KIAA0070 gene complete cds
32178	27	AA065507	Hs 97901	ESTs
32179	27	AA065508	Hs 97901	ESTs
32463	27	121887	Hs 121803	Human mRNA for KIAA0070 gene complete cds
34501	27	AA043768	Hs 13223	ESTs
13373	27	AA043770	Hs 13223	ESTs
6494	27	AA043660	Hs 34753	ESTs
10770	27	AA025771	Hs 103368	ESTs
10670	27	AA025772	Hs 103368	ESTs
11300	27	G1332-H13328	Hs 300708	EST - H03332-H13328
2319	27	M16127	Hs 819	Human home box c1 gene mRNA complete cds
18308	27	F10868	Hs 48371	Human GH3 domain-containing protein SH-UP18 mRNA complete cds
24190	27	AA091253	Hs 97101	ESTs
41955	27	T33111	Hs 2261	Neuronal pentamer II
34688	27	U10060	Hs 611	Human c-myc 3' UTR-associated protein 1 (HAP1.3) mRNA complete cds
1385	27	G184-H184	Hs 878	EST - H0884-H184
24758	27	Z60075	Hs 17595	ESTs
7820	27	AA182454	Hs 82868	ESTs, Moderately similar to C-1: TETRAHYDROGLUTE SYNTHASE CYTOSOLIC (H sapiens)
20720	27	H02078	Hs 13904	Human aspartate aminotransferase (EPR2) protein complete cds
21156	27	H03195	Hs 88013	Human aspartate aminotransferase (EPR2) protein complete cds
25585	27	AA045383	Hs 12719	UTRAN KOPPELLENT 2 (UTRAN2) mRNA complete cds
8298	27	004275	Hs 10724	ESTs, Moderately similar to C-1: TETRAHYDROGLUTE SYNTHASE CYTOSOLIC (H sapiens)
13174	27	AA021138	Hs 26750	ESTs
35357	27	AA048783	Hs 103285	ESTs
3154	27	H03712	Hs 8414	Chromogranin receptor, nuclear alpha polypeptide 3
1823	27	AA020334	Hs 105122	ESTs, Moderately similar to C-1: TETRAHYDROGLUTE SYNTHASE CYTOSOLIC (H sapiens)
24908	27	Z18160	Hs 8817	ESTs
35407	27	H45882	Hs 48572	ESTs
24728	27	AA037278	Hs 87721	ESTs
25408	27	H03787	Hs 23374	ESTs
26396	27	AA020334	Hs 105122	ESTs
18822	27	H03844	Hs 13173	ESTs
12378	27	AA039418	Hs 22170	Human aspartate aminotransferase (EPR2) protein complete cds
22888	27	R03287	Hs 25406	ESTs
24181	27	V020915	Hs 34820	ESTs

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FIGURE 3 (CONT.)

9538	9538	Hs 10203	ESTs	
24822	24822	Hs 10203	ESTs	
42028	42028	Hs 20701	ESTs	
6865	6865	Hs 8236	ESTs	
22148	22148	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
4517	4517	Hs 25029	ESTs	
9539	9539	Hs 84175	Human Hsp18 mRNA, complete cds	
25027	25027	Hs 25029	ESTs	
4102	4102	Hs 25029	ESTs	
612	612	Hs 38715	ESTs	
4321	4321	Hs 14670	Human mRNA for KIAA0148 gene (KIAA0148 protein)	
16007	16007	Hs 43136	ESTs	
15288	15288	Hs 43136	ESTs	
23322	23322	Hs 43136	ESTs	
10931	10931	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
6100	6100	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
39336	39336	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
17792	17792	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
4517	4517	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
2115	2115	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
10942	10942	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
19028	19028	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
7899	7899	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
8343	8343	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
10938	10938	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
11038	11038	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
4006	4006	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
36815	36815	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
11819	11819	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
37433	37433	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
42028	42028	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
18841	18841	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
10935	10935	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
14023	14023	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
31574	31574	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
7814	7814	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
17119	17119	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
7020	7020	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
17822	17822	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
24218	24218	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
19010	19010	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
17119	17119	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
30982	30982	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
8158	8158	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
17362	17362	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
8913	8913	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
13969	13969	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
32820	32820	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
22148	22148	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
11337	11337	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
29555	29555	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
29557	29557	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
27330	27330	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
17792	17792	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
14023	14023	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	
29522	29522	Hs 102178	Human mRNA for KIAA0261 gene (KIAA0261 protein)	

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FIGURE 3 (CONT.)

31	H11297	Hs131060	EST1	
32	H130032	EST1		
33	W27451	Hs17467	EST1	Moderately similar to PITG gene product (R. norvegicus)
34	W171832	Hs12064	Human Cdc-42-related protein (PCDC5/HRP) mRNA, complete cds	
35	W17524	Hs17960	EST1	
36	W17524	Hs17960	EST1	Human protein-tyrosine phosphatase (Hc-PP-1) mRNA, partial sequence
37	W17524	Hs17960	EST1	
38	Hs12350	EST1		Wt17524
39	Hs12350	EST1		Wt17524
40	Hs12350	EST1		Wt17524
41	Hs12350	EST1		Wt17524
42	Hs12350	EST1		Wt17524
43	Hs12350	EST1		Wt17524
44	Hs12350	EST1		Wt17524
45	Hs12350	EST1		Wt17524
46	Hs12350	EST1		Wt17524
47	Hs12350	EST1		Wt17524
48	Hs12350	EST1		Wt17524
49	Hs12350	EST1		Wt17524
50	Hs12350	EST1		Wt17524
51	Hs12350	EST1		Wt17524
52	Hs12350	EST1		Wt17524
53	Hs12350	EST1		Wt17524
54	Hs12350	EST1		Wt17524
55	Hs12350	EST1		Wt17524
56	Hs12350	EST1		Wt17524
57	Hs12350	EST1		Wt17524
58	Hs12350	EST1		Wt17524
59	Hs12350	EST1		Wt17524
60	Hs12350	EST1		Wt17524
61	Hs12350	EST1		Wt17524
62	Hs12350	EST1		Wt17524
63	Hs12350	EST1		Wt17524
64	Hs12350	EST1		Wt17524
65	Hs12350	EST1		Wt17524
66	Hs12350	EST1		Wt17524
67	Hs12350	EST1		Wt17524
68	Hs12350	EST1		Wt17524
69	Hs12350	EST1		Wt17524
70	Hs12350	EST1		Wt17524
71	Hs12350	EST1		Wt17524
72	Hs12350	EST1		Wt17524
73	Hs12350	EST1		Wt17524
74	Hs12350	EST1		Wt17524
75	Hs12350	EST1		Wt17524
76	Hs12350	EST1		Wt17524
77	Hs12350	EST1		Wt17524
78	Hs12350	EST1		Wt17524
79	Hs12350	EST1		Wt17524
80	Hs12350	EST1		Wt17524
81	Hs12350	EST1		Wt17524
82	Hs12350	EST1		Wt17524
83	Hs12350	EST1		Wt17524
84	Hs12350	EST1		Wt17524
85	Hs12350	EST1		Wt17524
86	Hs12350	EST1		Wt17524
87	Hs12350	EST1		Wt17524
88	Hs12350	EST1		Wt17524
89	Hs12350	EST1		Wt17524
90	Hs12350	EST1		Wt17524
91	Hs12350	EST1		Wt17524
92	Hs12350	EST1		Wt17524
93	Hs12350	EST1		Wt17524
94	Hs12350	EST1		Wt17524
95	Hs12350	EST1		Wt17524
96	Hs12350	EST1		Wt17524
97	Hs12350	EST1		Wt17524
98	Hs12350	EST1		Wt17524
99	Hs12350	EST1		Wt17524
100	Hs12350	EST1		Wt17524

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FIGURE 3 (CONT.)

Accession	Gene	Protein	Function
U00001	EST: RC_A432939	EST	
U00002	EST: RC_A432939	EST	
U00003	EST: RC_A432939	EST	
U00004	EST: RC_A432939	EST	
U00005	EST: RC_A432939	EST	
U00006	EST: RC_A432939	EST	
U00007	EST: RC_A432939	EST	
U00008	EST: RC_A432939	EST	
U00009	EST: RC_A432939	EST	
U00010	EST: RC_A432939	EST	
U00011	EST: RC_A432939	EST	
U00012	EST: RC_A432939	EST	
U00013	EST: RC_A432939	EST	
U00014	EST: RC_A432939	EST	
U00015	EST: RC_A432939	EST	
U00016	EST: RC_A432939	EST	
U00017	EST: RC_A432939	EST	
U00018	EST: RC_A432939	EST	
U00019	EST: RC_A432939	EST	
U00020	EST: RC_A432939	EST	
U00021	EST: RC_A432939	EST	
U00022	EST: RC_A432939	EST	
U00023	EST: RC_A432939	EST	
U00024	EST: RC_A432939	EST	
U00025	EST: RC_A432939	EST	
U00026	EST: RC_A432939	EST	
U00027	EST: RC_A432939	EST	
U00028	EST: RC_A432939	EST	
U00029	EST: RC_A432939	EST	
U00030	EST: RC_A432939	EST	
U00031	EST: RC_A432939	EST	
U00032	EST: RC_A432939	EST	
U00033	EST: RC_A432939	EST	
U00034	EST: RC_A432939	EST	
U00035	EST: RC_A432939	EST	
U00036	EST: RC_A432939	EST	
U00037	EST: RC_A432939	EST	
U00038	EST: RC_A432939	EST	
U00039	EST: RC_A432939	EST	
U00040	EST: RC_A432939	EST	
U00041	EST: RC_A432939	EST	
U00042	EST: RC_A432939	EST	
U00043	EST: RC_A432939	EST	
U00044	EST: RC_A432939	EST	
U00045	EST: RC_A432939	EST	
U00046	EST: RC_A432939	EST	
U00047	EST: RC_A432939	EST	
U00048	EST: RC_A432939	EST	
U00049	EST: RC_A432939	EST	
U00050	EST: RC_A432939	EST	
U00051	EST: RC_A432939	EST	
U00052	EST: RC_A432939	EST	
U00053	EST: RC_A432939	EST	
U00054	EST: RC_A432939	EST	
U00055	EST: RC_A432939	EST	
U00056	EST: RC_A432939	EST	
U00057	EST: RC_A432939	EST	
U00058	EST: RC_A432939	EST	
U00059	EST: RC_A432939	EST	
U00060	EST: RC_A432939	EST	
U00061	EST: RC_A432939	EST	
U00062	EST: RC_A432939	EST	
U00063	EST: RC_A432939	EST	
U00064	EST: RC_A432939	EST	
U00065	EST: RC_A432939	EST	
U00066	EST: RC_A432939	EST	
U00067	EST: RC_A432939	EST	
U00068	EST: RC_A432939	EST	
U00069	EST: RC_A432939	EST	
U00070	EST: RC_A432939	EST	
U00071	EST: RC_A432939	EST	
U00072	EST: RC_A432939	EST	
U00073	EST: RC_A432939	EST	
U00074	EST: RC_A432939	EST	
U00075	EST: RC_A432939	EST	
U00076	EST: RC_A432939	EST	
U00077	EST: RC_A432939	EST	
U00078	EST: RC_A432939	EST	
U00079	EST: RC_A432939	EST	
U00080	EST: RC_A432939	EST	
U00081	EST: RC_A432939	EST	
U00082	EST: RC_A432939	EST	
U00083	EST: RC_A432939	EST	
U00084	EST: RC_A432939	EST	
U00085	EST: RC_A432939	EST	
U00086	EST: RC_A432939	EST	

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FIGURE 3 (CONT.)

[illegible]

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FIGURE 3 (CONT.)

1252	33	AA454403	Hs 28511	ESTs	Modestly similar to YYY-esterase-like-2 (Hs sapiens)
1253	33	AA454403	Hs 28511	ESTs	Modestly similar to YYY-esterase-like-2 (Hs sapiens)
26853	33	AA237374	Hs 142497	ESTs	
37434	33	AA424149	Hs 98357	ESTs	
7833	33	AA245300	Hs 7048	ESTs	
3874	33	U53337	Hs 98822	Human testis 50 nucleosome 1 (FAC-1) mRNA complete cds	
32674	33	U53373	Hs 71823	ESTs	
32674	33	AA454403	Hs 28511	ESTs	Modestly similar to YYY-esterase-like-2 (Hs sapiens)
19177	33	AA245300	Hs 7048	ESTs	
19179	33	AA245300	Hs 7048	ESTs	
3846	33	U53337	Hs 98822	ESTs	
42097	33	U53337	Hs 98822	ESTs	
24247	33	U53337	Hs 98822	ESTs	
42097	33	U53337	Hs 98822	ESTs	
5078	33	U53337	Hs 98822	ESTs	
23235	33	U53337	Hs 98822	ESTs	
3971	33	U53337	Hs 98822	ESTs	
3239	33	U53337	Hs 98822	ESTs	
41987	33	U53337	Hs 98822	ESTs	
31105	33	U53337	Hs 98822	ESTs	
31105	33	U53337	Hs 98822	ESTs	
7654	33	U53337	Hs 98822	ESTs	
6338	33	U53337	Hs 98822	ESTs	
20263	33	U53337	Hs 98822	ESTs	
14539	33	U53337	Hs 98822	ESTs	
21187	33	U53337	Hs 98822	ESTs	
33320	33	U53337	Hs 98822	ESTs	
41825	33	U53337	Hs 98822	ESTs	
4574	33	U53337	Hs 98822	ESTs	
79481	33	U53337	Hs 98822	ESTs	
21082	33	U53337	Hs 98822	ESTs	
21082	33	U53337	Hs 98822	ESTs	
11497	33	U53337	Hs 98822	ESTs	
23500	33	U53337	Hs 98822	ESTs	
41835	33	U53337	Hs 98822	ESTs	
28875	33	U53337	Hs 98822	ESTs	
42585	33	U53337	Hs 98822	ESTs	
3423	33	U53337	Hs 98822	ESTs	
42585	33	U53337	Hs 98822	ESTs	
3537	33	U53337	Hs 98822	ESTs	
21241	33	U53337	Hs 98822	ESTs	
23756	33	U53337	Hs 98822	ESTs	
34104	33	U53337	Hs 98822	ESTs	
88172	33	U53337	Hs 98822	ESTs	
28872	33	U53337	Hs 98822	ESTs	
19516	33	U53337	Hs 98822	ESTs	
72543	33	U53337	Hs 98822	ESTs	
10054	33	U53337	Hs 98822	ESTs	
34094	33	U53337	Hs 98822	ESTs	
21082	33	U53337	Hs 98822	ESTs	
21082	33	U53337	Hs 98822	ESTs	
19836	33	U53337	Hs 98822	ESTs	
34568	33	U53337	Hs 98822	ESTs	
28448	33	U53337	Hs 98822	ESTs	
28872	33	U53337	Hs 98822	ESTs	
40128	33	U53337	Hs 98822	ESTs	
20240	33	U53337	Hs 98822	ESTs	

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FIGURE 3 (CONT.)

[illegible]

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FIGURE 3 (CONT.)

4225	21	U39452	EST - U39453	EST - U39454	EST - U39455
37415	21	AA431807	Hs 39149	EST	EST
14163	21	AA421310	Hs 10500	ESTs Weakly similar to HYPOPHOSPHATE-39 K D PROTEIN IN WIDELIUMPH13 INTERGENIC REGION [Rozdzinski et al. 1994]	
27756	21	AA423417	Hs 34421	ESTs	
17377	21	AA437145	Hs 31171	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
5173	21	U81534	Hs 15322	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
17379	21	U81535	Hs 15323	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
19917	21	U81536	Hs 15324	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
22501	21	U81537	Hs 15325	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
22504	21	U81538	Hs 15326	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
40143	21	U81539	Hs 15327	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
3481	21	U81540	Hs 15328	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
11880	21	U81541	Hs 15329	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
30071	21	U81542	Hs 15330	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
8382	21	AA424198	Hs 3589	ESTs Weakly similar to TRANSGLUTAMINATION SENSITIVE PROTEIN RE-ESP 3521 (H. sapiens)	
23229	21	AA424199	Hs 3591	ESTs Weakly similar to TRANSGLUTAMINATION SENSITIVE PROTEIN RE-ESP 3521 (H. sapiens)	
5807	21	U81543	Hs 3592	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
19147	21	U81544	Hs 3593	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
2815	21	U81545	Hs 3594	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
5210	21	U81546	Hs 3595	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
9144	21	U81547	Hs 3596	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
25165	21	AA424232	Hs 81725	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
23418	21	AA424233	Hs 81726	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
1401	21	U81548	Hs 81727	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
5211	21	U81549	Hs 81728	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
10898	21	AA424234	Hs 81729	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
381	21	AA424235	Hs 81730	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
22051	21	AA424236	Hs 81731	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
22979	21	AA424237	Hs 81732	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
12018	21	AA424238	Hs 81733	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
11000	21	AA424239	Hs 81734	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
13843	21	AA424240	Hs 81735	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
19917	21	AA424241	Hs 81736	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
30511	21	AA424242	Hs 81737	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
21309	21	AA424243	Hs 81738	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
21153	21	AA424244	Hs 81739	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
33066	21	AA424245	Hs 81740	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
7525	21	AA424246	Hs 81741	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
39592	21	AA424247	Hs 81742	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
28079	21	AA424248	Hs 81743	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
18425	21	AA424249	Hs 81744	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
23844	21	AA424250	Hs 81745	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
32997	21	AA424251	Hs 81746	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
32368	21	AA424252	Hs 81747	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
10258	21	AA424253	Hs 81748	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
21882	21	AA424254	Hs 81749	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
20980	21	AA424255	Hs 81750	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
22901	21	AA424256	Hs 81751	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
42044	21	AA424257	Hs 81752	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
4210	21	AA424258	Hs 81753	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
31	21	AA424259	Hs 81754	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
14300	21	AA424260	Hs 81755	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
23180	21	AA424261	Hs 81756	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
23190	21	AA424262	Hs 81757	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	
24071	21	AA424263	Hs 81758	Homo sapiens signal recognition particle 71 (SRP72) mRNA complete cds	

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FIGURE 3 (CONT.)

8115	20	AA32593	Hs 10458	EST
8122	20	AA32593	Hs 10458	EST
8123	20	AA32593	Hs 10458	EST
8124	20	AA32593	Hs 10458	EST
8125	20	AA32593	Hs 10458	EST
8126	20	AA32593	Hs 10458	EST
8127	20	AA32593	Hs 10458	EST
8128	20	AA32593	Hs 10458	EST
8129	20	AA32593	Hs 10458	EST
8130	20	AA32593	Hs 10458	EST
8131	20	AA32593	Hs 10458	EST
8132	20	AA32593	Hs 10458	EST
8133	20	AA32593	Hs 10458	EST
8134	20	AA32593	Hs 10458	EST
8135	20	AA32593	Hs 10458	EST
8136	20	AA32593	Hs 10458	EST
8137	20	AA32593	Hs 10458	EST
8138	20	AA32593	Hs 10458	EST
8139	20	AA32593	Hs 10458	EST
8140	20	AA32593	Hs 10458	EST
8141	20	AA32593	Hs 10458	EST
8142	20	AA32593	Hs 10458	EST
8143	20	AA32593	Hs 10458	EST
8144	20	AA32593	Hs 10458	EST
8145	20	AA32593	Hs 10458	EST
8146	20	AA32593	Hs 10458	EST
8147	20	AA32593	Hs 10458	EST
8148	20	AA32593	Hs 10458	EST
8149	20	AA32593	Hs 10458	EST
8150	20	AA32593	Hs 10458	EST
8151	20	AA32593	Hs 10458	EST
8152	20	AA32593	Hs 10458	EST
8153	20	AA32593	Hs 10458	EST
8154	20	AA32593	Hs 10458	EST
8155	20	AA32593	Hs 10458	EST
8156	20	AA32593	Hs 10458	EST
8157	20	AA32593	Hs 10458	EST
8158	20	AA32593	Hs 10458	EST
8159	20	AA32593	Hs 10458	EST
8160	20	AA32593	Hs 10458	EST
8161	20	AA32593	Hs 10458	EST
8162	20	AA32593	Hs 10458	EST
8163	20	AA32593	Hs 10458	EST
8164	20	AA32593	Hs 10458	EST
8165	20	AA32593	Hs 10458	EST
8166	20	AA32593	Hs 10458	EST
8167	20	AA32593	Hs 10458	EST
8168	20	AA32593	Hs 10458	EST
8169	20	AA32593	Hs 10458	EST
8170	20	AA32593	Hs 10458	EST
8171	20	AA32593	Hs 10458	EST
8172	20	AA32593	Hs 10458	EST
8173	20	AA32593	Hs 10458	EST
8174	20	AA32593	Hs 10458	EST
8175	20	AA32593	Hs 10458	EST
8176	20	AA32593	Hs 10458	EST
8177	20	AA32593	Hs 10458	EST
8178	20	AA32593	Hs 10458	EST
8179	20	AA32593	Hs 10458	EST
8180	20	AA32593	Hs 10458	EST
8181	20	AA32593	Hs 10458	EST
8182	20	AA32593	Hs 10458	EST
8183	20	AA32593	Hs 10458	EST
8184	20	AA32593	Hs 10458	EST
8185	20	AA32593	Hs 10458	EST
8186	20	AA32593	Hs 10458	EST
8187	20	AA32593	Hs 10458	EST
8188	20	AA32593	Hs 10458	EST
8189	20	AA32593	Hs 10458	EST
8190	20	AA32593	Hs 10458	EST
8191	20	AA32593	Hs 10458	EST
8192	20	AA32593	Hs 10458	EST
8193	20	AA32593	Hs 10458	EST
8194	20	AA32593	Hs 10458	EST
8195	20	AA32593	Hs 10458	EST
8196	20	AA32593	Hs 10458	EST
8197	20	AA32593	Hs 10458	EST
8198	20	AA32593	Hs 10458	EST
8199	20	AA32593	Hs 10458	EST
8200	20	AA32593	Hs 10458	EST

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FIGURE 4

Primary Key	NC number of nucleotides in sequence	Accession	Unigene Cluster	Unigene Description
32516	>10	U02170	Hs15079	Protease inhibitor 3 (trypsin)
34197	>10	AA232315	Hs12540	Human spleen clone 23797 and 23317 mRNA, part 1 cds
19387	>10	U02128	Hs31656	ESTs
8125	>10	AA330771	Hs12911	Human protein-tyrosine phosphatase (Hs pp-1) mRNA partial sequence
18362	>10	AA232312	Hs12013	Ribonuclease L (2S -diphosphorylated synthetase dependent) inhibitor
39935	>10	H62474	Hs10240	EST
39228	>10	H117898	Hs22659	ESTs
39228	>10	AA358648	Hs72202	Human mRNA for transcriptional activator HNF2B complete cds
38456	>10	AA358648	Hs72202	Human mRNA for transcriptional activator HNF2B complete cds
17659	>10	AA328402	Hs71990	ESTs
6106	>10	X70953	Hs18414	SRV (has cleaving region Y) cont. 4
8948	>10	AA485018	Hs18413	Human spleen cDNA protease (has 1) mRNA complete cds
5918	>10	X14850	Hs2711	HISTONE H2A.X
5903	>10	X14353	Hs75581	Transcription factor 1
37877	>10	AA460530	Hs18234	Human spleen cDNA protease (has 1) mRNA complete cds
11581	>10	AA236533	Hs19222	E4-1
18430	>10	AA078418	Hs19153	ESTs
32240	>10	H50076	Hs12013	Ribonuclease L (2S -diphosphorylated synthetase dependent) inhibitor
12425	>10	AA403116	Hs18800	Human spleen U-methyl-lysine-associated cytoplasm (Hs U-methyl-lysine) mRNA complete cds
2114	>10	X14316	Hs74094	Proteinase C beta 4
1214	>10	AA460530	Hs18234	Human spleen cDNA protease (has 1) mRNA complete cds
33055	>10	U02128	Hs31656	ESTs
8449	>10	X99536	Hs11860	ESTs
37853	>10	AA460517	Hs32930	Human spleen cDNA protease (has 1) mRNA complete cds
4178	>10	U30746	Hs110756	Human bursin-like Na-K-ATPase (Hs Na-K-ATPase) mRNA complete cds
1863	>10	L16161	Hs171541	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT
19787	>10	H56079	Hs37362	ESTs
8292	>10	AA318272	Hs24550	ESTs
10747	>10	AA358641	Hs31853	ESTs
6212	>10	U02128	Hs31656	ESTs
33191	>10	X70953	Hs18414	SRV (has cleaving region Y) cont. 4
6183	>10	AA328402	Hs71990	ESTs
13136	>10	X99536	Hs11860	ESTs
5903	>10	X99536	Hs11860	ESTs
38179	>10	AA487492	Hs2377	Calcium 3 (p-calcin)
30238	>10	H50561	Hs78272	Human spleen clone 23592 mRNA sequence
17887	>10	AA189319	Hs184586	Cathepsin B
36095	>10	AA433910	Hs72853	ESTs
10233	>10	H71427	Hs18786	ESTs
38330	>10	AA460530	Hs10091	ESTs
38456	>10	AA358648	Hs72202	Human mRNA for transcriptional activator HNF2B complete cds
38456	>10	AA358648	Hs72202	Human mRNA for transcriptional activator HNF2B complete cds
5910	>10	X70953	Hs18414	SRV (has cleaving region Y) cont. 4
3021	>10	M6841	Hs131015	EST - Hs131015-155
17734	>10	AA137240	Hs131015	EST - Hs131015-155
36371	>10	AA425017	Hs131015	EST - Hs131015-155
459	>10	D3893	Hs73876	Cell division cycle 2 C1 10.5 and C2 10.6
17419	>10	AA113349	Hs184586	Cathepsin B
14054	>10	AA485323	Hs72853	ESTs
5021	>10	U73324	Hs18786	ESTs
4964	>10	U72314	Hs17005	Human C2 mRNA complete cds

FIGURE 4 (CONT.)

23355	AA256378	Hs 99281	ESTs
4445	U0844	Hs 14732	MALATE OXIDOREDUCTASE
10748	AA055692	Hs 14543	ESTs
8111	AA323787	Hs 4770	ESTs
19289	H20185	Hs 31724	EST
32195	H43471	Hs 23255	ESTs Weakly similar to ORF YOR259a (S cerevisiae)
21519	R77975	EST - HC_R27975	
6197	R77975	Hs 12013	Ribonuclease L (2S of poliovirus RNA synthesis dependent) inhibitor
5986	RG1834	Hs 11878	ESTs
41107	AA324963	Hs 10989	Estrogen corepressor and ubiquitin type 1
10748	U0844	Hs 10989	ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR (Rattus norvegicus)
19078	U0844	EST - U0844	
19078	FR022	Hs 27895	ESTs
24197	V07277	Hs 17648	ESTs
4713	U57771	Hs 81771	Human L-lysine hydrolase mRNA complete cds
34460	AA504462	Hs 105730	ESTs
18330	AA318722	Hs 54481	Human mRNA for apolipoprotein E receptor 2 complete cds
18182	F09739	Hs 12369	ESTs
42766	Z09394	Hs 84432	ESTs Moderately similar to H1ALU SUBFAMILY SP REPEATING ENTRY (H1A species)
34014	AA191348	Hs 80178	ESTs
18935	AA054585	Hs 42106	ESTs
11165	HC2003	Hs 42106	ESTs
11165	AA184589	Hs 26008	ESTs
11165	HQ3044473521	EST - HQ33444-H1351	
11813	AA059168	Hs 22163	ESTs
10992	AA112523	Hs 22200	Human apurine BAC clone RG11602 from Tp15
5789	X54925	Hs 83769	Human metallothionein 1 (intracisternal cognate)
16993	AA095300	Hs 75337	Human mRNA for KIAA0025 gene partial cds
17654	AA193250	Hs 09180	ESTs
39436	D26927	Hs 74374	Human Cdk- dependent endonuclease protein for secretion mRNA complete cds
19277	R27622	Hs 25851	ESTs
4331	R27622	Hs 31748	Human mRNA for IRE5
17516	R79111	Hs 29398	ESTs
32708	AA06206	Hs 104746	ESTs
32980	AA180223	Hs 8414	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN
37084	AA464869	Hs 175179	Human insulin like binding protein 2 (IRBP2) gene partial cds
25935	AA347199	Hs 77831	ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (Ceratobasidium elegans)
2188	L47276	EST - L47276	
4362	U09617	Hs 30229	Bloom syndrome
9127	D30037	Hs 91447	PHOSPHATIDYLINOSITOL
20914	N39230	Hs 18937	ESTs
5932	U07044	Hs 10970	Human Cdk- dependent endonuclease protein for secretion mRNA complete cds
3288	U07114	Hs 10981	Human Cdk- dependent endonuclease protein for secretion mRNA complete cds
21445	U01157	Hs 185	Quadruplex peptide-1 receptor
37455	Z38482	Hs 12403	ESTs
37455	AA454932	Hs 123157	ESTs
10840	AA084104	Hs 30177	ESTs
23179	AA037268	Hs 113379	Human mRNA for synectin-2
21	AB000265	Hs 143080	Human insulin like binding protein 2 (IRBP2) gene partial cds
18782	F09458	Hs 12421	ESTs
39232	AA011409	Hs 117958	ESTs
42602	AF054215	Hs 117958	ESTs
23272	R054215	Hs 117958	ESTs
18410	AA030709	Hs 20593	ESTs Weakly similar to HYPOPHYSICAL WP B KD PROTEIN 1051167 IN CHROMOSOME II (C. elegans)
23845	AA030836	Hs 120849	ESTs
	H52940	Hs 42116	ESTs

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FIGURE 4 (CONT.)

36425	AA426405	Hs 10801	Homo sapiens mRNA for KIAA0530 protein partial cds
4029	U21099	Hs 74590	Human DNA polymerase delta small subunit mRNA complete cds
15056	U07246	Hs 110729	Human tumour necrosis factor alpha mRNA complete cds
40594	N35388	Hs 112227	EST
31484	M89456	Hs 49593	EST
36201	AA395335	Hs 105041	EST
32071	U13814	Hs 98581	EST
236	D13644	Hs 67071	Human mRNA for KIAA0020 gene complete cds
35803	AA107955	Hs 67911	EST
10593	H40268	Hs 33765	EST
36229	AA609177	Hs 106953	EST
35786	AA410231	Hs 58069	EST
3183	M84474	Hs 1355	Cathepsin E
22400	R64109	Hs 26487	EST
35652	AA620333	Hs 112837	EST
25052	AA017257	Hs 101139	EST
5957	X59377	Hs 11721	Human mRNA for angiogenesis inhibitor factor
5214	U03323	Hs 125029	Human mRNA for granulocyte chemotactic protein
40546	AA416500	Hs 11709	EST
25851	AA01504	Hs 7016	NECLAR FACTOR RPR-40
22072	R49406	Hs 134158	EST
36837	H36279	Hs 26410	EST
23186	T40530	Hs 8241	EST, RC, H36279
29331	M83116	Hs 39093	EST
35316	AA492500	Hs 18247	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds
27629	AA470504	Hs 89558	EST
36176	U141518	Hs 9564	Estrogen receptor protein A (17.0)
41775	AA050571	Hs 7297	EST
32277	R81463	Hs 73927	EST
3558	X07676	Hs 25986	Human mRNA for rod photoreceptor protein complete cds
6382	X51133	Hs 83761	Winged-type LIM/TV integration site 2 human homolog
41040	N81948	Hs 65273	Human RBC-1 mRNA
30060	AA625352	Hs 125024	EST
70207	N24430	Hs 7202	EST, RC, AA625352
16790	AA306901	Hs 37036	EST
41085	N26218	Hs 68377	EST
32109	V52291	Hs 28554	EST
36110	AA417711	Hs 22564	Human mRNA for KIAA0359 gene complete cds
36815	N50138	Hs 11800	EST
40359	N33024	Hs 10984	EST
1445	J03077	Hs 23450	EST
37883	AA445594	Hs 73895	MHC class I protein HLA-G
42742	T89579	Hs 21331	EST
37135	AA412540	Hs 52871	Human mRNA for SYT
2664	N56443	Hs 79353	Human apolipoprotein E3-related transcription factor (DP-1) mRNA complete cds
31615	AA465327	Hs 69112	EST
21240	R06613	Hs 125925	EST
34382	AA325512	Hs 20168	EST
25948	AA324355	Hs 10098	EST
42013	N92218	Hs 102459	Homo sapiens survival of motor neuron protein interacting protein 1 (SP1) mRNA complete cds
35897	AA405512	Hs 106233	EST
34672	AA324372	Hs 13474	EST
		Hs 111471	EST

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FIGURE 4 (CONT.)

26528	10	A428041	Hs 40128 ESTs highly similar to GOS RIBOSOMAL PROTEIN L30 (ratia nervosa)
40704	10	H8396	EST - RC_H8396
19164	10	H10395	EST
26240	10	Hs 90439	Human mRNA for KIAA0152 gene complete cds
6963	10	A232382	AFK-HUMIT RRM11507_M
33372	10	AQ328710	Hs 87195 H. sapiens RNA for CLON5
27293	10	Hs 87195	EST - HQ37-H137
36052	10	Hs 35533	EST
26514	10	Hs 104707	EST
33197	10	Hs 88529	ESTs
37978	10	Hs 97504	ESTs
4862	10	A417625	Hs 106200 ESTs highly similar to RING CANAL PROTEIN (Drosophila melanogaster)
26700	10	U65437	Hs 85808 Human homeodomain-containing protein (HNF) mRNA complete cds
35049	10	A232197	EST
40063	10	H72596	ESTs
17041	10	A127459	Hs 76086 MITOCHONDRIAL GOS RIBOSOMAL PROTEIN L3
4477	10	U65865	ESTs
26916	10	U65865	Hs 116151 ESTs highly similar to HNF-1A2 gene protein LIP mRNA complete cds
34185	10	A2331363	Hs 42378 ESTs
27229	10	A279630	Hs 102524 ESTs
42773	10	H49458	Human mRNA for KIAA0186 gene complete cds
32185	10	YEL019C/M321	EST - YEL019C/M321
36739	10	R43183	EST - RC_AA43510
26545	10	H56931	EST
21822	10	A278979	EST
26545	10	R43622	EST
22044	10	A436046	Hs 26491 ESTs highly similar to CYCLIC AMP DEPENDENT TRANSCRIPTION FACTOR ATF-2 (H. sapiens)
1346	10	HQ4718-H15158	EST - HQ4718/H15158
218	10	D13540	Hs 22968 PROTEIN-TYROSINE PHOSPHATASE 2C
26100	10	A242835	Hs 5917 Human mRNA for KIAA0337 gene complete cds
41583	10	B64129	Hs 143745 ESTs
42200	10	T66105	Hs 142670 ESTs
6713	10	Y06564	EST - Y06564
33027	10	Y06564	ESTs highly similar to F46B17 (C. elegans)
31819	10	N73449	Hs 52273 ESTs
26718	10	A232576	Hs 40407 ESTs
26718	10	H73512	Hs 104859 Human A1 8 mRNA complete cds
40113	10	H73512	ESTs
10801	10	A209285	Hs 9722 ESTs highly similar to PROBABLE UBQUITIN-CARBOXYL-TERMINAL HYDROLASE 9 (Hs 11.3 (C. elegans))
37491	10	A4455239	Hs 97630 ESTs highly similar to CHROMOSOME CONDENSATION PROTEIN Dp1.27 (Caenorhabditis elegans)
254	10	D14627	Hs 81892 Human mRNA for KIAA0101 gene complete cds
26893	10	H97819	Hs 42453 ESTs
21523	10	A278382	Hs 43881 ESTs
13110	10	A4435640	Hs 19114 Homo sapiens mRNA for high mobility group protein HMG2a
34963	10	A2397764	Hs 80041 EST
31427	10	D51691	Hs 82205 Phosphoribosylpyrimidine 5-triphosphatase 5-phosphoribosylpyrimidine synthetase phosphoribosyl aminimidate synthetase
21522	10	N71274	Hs 110244 ESTs
20342	10	A436046	ESTs
4476	10	U65008	Hs 78619 Homo sapiens gamma-glutamyl hydrolase (GGH) mRNA complete cds
34363	10	A2351587	Hs 10901 Homo sapiens mRNA for KIAA0330 protein partial cds
35094	10	A436046	ESTs
3688	10	U15128	Hs 30573 Human beta-12-N-acetylglucosaminyltransferase II (MUCAT2) gene complete cds

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FIGURE 4 (CONT.)

32386	02184	Hs 3350	ESTs	Hs 3350	ESTs
4187	U1759	Hs 121479	Human 9P antisense receptor (PTGDR) mRNA partial cds	Hs 121479	Human 9P antisense receptor (PTGDR) mRNA partial cds
4507	U1759	Hs 24852	Human putative calcium efflux channel (hac3) mRNA complete cds	Hs 24852	Human putative calcium efflux channel (hac3) mRNA complete cds
35606	AA402227	Hs 97345	ESTs	Hs 97345	ESTs
18219	Hs 58413	Hs 37629	EST	Hs 37629	EST
14837	T40145	Hs 21821	ESTs	Hs 21821	ESTs
17336	AA099555	Hs 41175	ESTs	Hs 41175	ESTs
24066	Hs 54334	Hs 40972	EST	Hs 40972	EST
29943	Hs 42993	ESTs	Moderately similar to "H. ALU SUBFAMILY J WARRING ENTRY III" [H. sapiens]	Hs 42993	ESTs
17697	AA106833	Hs 72535	EST	Hs 72535	EST
13893	AA170817	Hs 34027	ESTs	Hs 34027	ESTs
26339	Hs 85928	ESTs	Weakly similar to No definition line found [C. elegans]	Hs 85928	ESTs
26363	AA327072	Hs 80369	ESTs	Hs 80369	ESTs
40074	Hs 83369	ESTs	Hs 83369	ESTs	
9031	Hs 96	ATI-derived PMA responsive (APR) peptide	Hs 96	ATI-derived PMA responsive (APR) peptide	
27674	Hs 33095	ESTs	Hs 33095	ESTs	
15244	W00304	Hs 8037	ESTs	Hs 8037	ESTs
18263	AA329457	Hs 82489	ESTs	Hs 82489	ESTs
19662	Hs 7381	Hs 33947	ESTs	Hs 33947	ESTs
2348	Hs 25937	Hs 81564	Phorbol factor 4	Hs 81564	Phorbol factor 4
7736	AA323121	Hs 109931	Human tyrosyl tRNA synthetase mRNA complete cds	Hs 109931	Human tyrosyl tRNA synthetase mRNA complete cds
39929	Hs 53454	Hs 110731	ESTs	Hs 110731	ESTs
25111	AA025187	Hs 10731	ESTs	Hs 10731	ESTs
21714	Hs 10731	ESTs	Hs 10731	ESTs	
27024	Hs 39753	ESTs	Weakly similar to C26B1.3 [C. elegans]	Hs 39753	ESTs
4999	AA401425	Hs 82925	Human transposon (TRN) mRNA complete cds	Hs 82925	Human transposon (TRN) mRNA complete cds
2316	U16322	EST - M14123_xpt	EST - M14123_xpt	EST - M14123_xpt	EST - M14123_xpt
37253	Hs 11731	ESTs	Hs 11731	ESTs	
38624	AA440337	Hs 131234	ESTs	Hs 131234	ESTs
23213	F10236	Hs 8330	ESTs	Hs 8330	ESTs
2790	T40591	Hs 2164	Connective tissue activation peptide III	Hs 2164	Connective tissue activation peptide III
32479	Hs 11632	Hs 73188	WEE-LIKE PROTEIN KINASE	Hs 73188	WEE-LIKE PROTEIN KINASE
19681	AA025187	Hs 39851	ESTs	Hs 39851	ESTs
21714	Hs 10731	ESTs	Weakly similar to RHOBTB1A-1 [H. sapiens]	Hs 10731	ESTs
14723	Hs 80345	Hs 10730	ESTs	Hs 10730	ESTs
31764	D59854	Hs 3782	ESTs	Hs 3782	ESTs
6069	AA447068	Hs 77204	Human CENP-F kinesin-like protein mRNA complete cds	Hs 77204	Human CENP-F kinesin-like protein mRNA complete cds
7465	AA133367	Hs 133101	Hs 133101	Hs 133101	Hs 133101
16501	AA178547	Hs 81686	ESTs	Hs 81686	ESTs
34327	AA025969	Hs 81423	ESTs	Hs 81423	ESTs
6700	AA027001	Hs 104420	ESTs	Hs 104420	ESTs
2632	T407617	Hs 35842	H. sapiens mRNA for Pim isolate 1	Hs 35842	H. sapiens mRNA for Pim isolate 1
11188	AA172222	Hs 91728	Human 75-kD autoantigen (PNA-Scl) mRNA complete cds	Hs 91728	Human 75-kD autoantigen (PNA-Scl) mRNA complete cds
42793	Hs 20058	ESTs	Hs 20058	ESTs	
18255	Hs 17575	ESTs	Weakly similar to C. elegans cDNA p1-102.3 [C. elegans]	Hs 17575	ESTs
23371	Hs 2246	EST - RC_159505	EST - RC_159505	EST - RC_159505	EST - RC_159505
17508	AA028201	Hs 92703	ESTs	Hs 92703	ESTs
18407	AA033793	Hs 65828	ESTs	Hs 65828	ESTs
235	O13844	Hs 140933	Human mRNA for KIAA0219 gene complete cds	Hs 140933	Human mRNA for KIAA0219 gene complete cds
24523	Z38347	Hs 118338	ESTs	Hs 118338	ESTs
7826	AA348584	Hs 123918	Homo sapiens clone 24540 mRNA sequence	Hs 123918	Homo sapiens clone 24540 mRNA sequence
37142	R39715	Hs 17260	ESTs	Hs 17260	ESTs
39007	AA020425	Hs 3115	Cosmon alpha S1	Hs 3115	Cosmon alpha S1
6235	X18416	Hs 78822	ESTs	Hs 78822	ESTs
24317	Hs 78822	ESTs	Moderately similar to isolation factor srf-26 gamma subunit [R. norvegicus]	Hs 78822	ESTs
38344	CT1334	CT1334	CT1334	CT1334	CT1334

FIGURE 4 (CONT.)

[illegible]

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FIGURE 4 (CONT.)

44	CD3098	Hs 04726	EST1
45	CD3098	Hs 23060	Cytidin B1
46	CD3098	Hs 73060	Nuclear factor of kappa B light polypeptide gene enhancer in B cells 2 (NF-kappa B2)
47	NB0904	Hs 91464	ESTs
48	NB0904	Hs 91464	ESTs
49	NB0904	Hs 91464	ESTs
50	NB0904	Hs 91464	ESTs
51	NB0904	Hs 91464	ESTs
52	NB0904	Hs 91464	ESTs
53	NB0904	Hs 91464	ESTs
54	NB0904	Hs 91464	ESTs
55	NB0904	Hs 91464	ESTs
56	NB0904	Hs 91464	ESTs
57	NB0904	Hs 91464	ESTs
58	NB0904	Hs 91464	ESTs
59	NB0904	Hs 91464	ESTs
60	NB0904	Hs 91464	ESTs
61	NB0904	Hs 91464	ESTs
62	NB0904	Hs 91464	ESTs
63	NB0904	Hs 91464	ESTs
64	NB0904	Hs 91464	ESTs
65	NB0904	Hs 91464	ESTs
66	NB0904	Hs 91464	ESTs
67	NB0904	Hs 91464	ESTs
68	NB0904	Hs 91464	ESTs
69	NB0904	Hs 91464	ESTs
70	NB0904	Hs 91464	ESTs
71	NB0904	Hs 91464	ESTs
72	NB0904	Hs 91464	ESTs
73	NB0904	Hs 91464	ESTs
74	NB0904	Hs 91464	ESTs
75	NB0904	Hs 91464	ESTs
76	NB0904	Hs 91464	ESTs
77	NB0904	Hs 91464	ESTs
78	NB0904	Hs 91464	ESTs
79	NB0904	Hs 91464	ESTs
80	NB0904	Hs 91464	ESTs
81	NB0904	Hs 91464	ESTs
82	NB0904	Hs 91464	ESTs
83	NB0904	Hs 91464	ESTs
84	NB0904	Hs 91464	ESTs
85	NB0904	Hs 91464	ESTs
86	NB0904	Hs 91464	ESTs
87	NB0904	Hs 91464	ESTs
88	NB0904	Hs 91464	ESTs
89	NB0904	Hs 91464	ESTs
90	NB0904	Hs 91464	ESTs
91	NB0904	Hs 91464	ESTs
92	NB0904	Hs 91464	ESTs
93	NB0904	Hs 91464	ESTs
94	NB0904	Hs 91464	ESTs
95	NB0904	Hs 91464	ESTs
96	NB0904	Hs 91464	ESTs
97	NB0904	Hs 91464	ESTs
98	NB0904	Hs 91464	ESTs
99	NB0904	Hs 91464	ESTs
100	NB0904	Hs 91464	ESTs

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FIGURE 4 (CONT.)

2345	W23753	Hs.23900	Cyclin B1
3352	W63127	Hs.59422	ESTs
28443	D60252	Hs.110619	ESTs
6160	X74794	Hs.80906	CD221 HOMOLOG
42515	W72110	Hs.100333	Homo sapiens clone 23822 mRNA sequence
3392	U25212	Hs.84713	Human histon H4 interacting protein (HIF2) mRNA complete cds
2320	U25212	Hs.84713	Human histon H4 interacting protein (HIF2) mRNA complete cds
20320	A439214	Hs.63370	ESTs
746	D84154	Hs.21890	Homo sapiens mRNA for LDP, cathepsin B activator complete cds
3117	M81182	Hs.7181	Transitional membrane protein 1 (TMD2) Zellerger syndrome
21257	R09186	Hs.20321	ESTs
31487	M69507	Hs.129649	ESTs
28954	F03153	Hs.80383	ESTs
38928	A4609565	Hs.106990	ESTs
22909	N33366	Hs.63664	ESTs
8470	A491250	Hs.54990	ESTs
9715	H46817	EST - H46817	
21411	H46817	EST - H46817	
30015	A428137	Hs.69434	ESTs
29934	N59146	Hs.47076	ESTs
1064	N24194	Hs.43551	ESTs
11222	HQ2945-HT2953	Hs.25740	ESTs
26343	AA188904	ESTs	Weakly similar to unknown (S. cerevisiae)
8035	AA267450	Hs.83842	ESTs
19293	AA305116	EST - AA305116	
24596	H15054	Hs.22184	ESTs
5960	C21245	Hs.27194	ESTs
30710	N51781	Hs.11171	Hs. sapiens mRNA for cytoplasmic specific protein
2350	A258460	Hs.42338	ESTs
30282	M15798	Hs.46810	ESTs
41792	T03886	Hs.78996	Proliferating cell nuclear antigen
42185	AA434411	Hs.44690	Homo sapiens clone 21739 mRNA sequence
35146	AA436968	Hs.100265	ESTs
29593	F79951	Hs.89800	ESTs
27117	F09134	Hs.11805	ESTs
33458	AA403003	Hs.12036	ESTs
26693	Hs.89003	ESTs	
12659	Hs.86178	Hs. sapiens mRNA for M-phase phosphoprotein mc29	
34028	U15178	Hs.81178	ESTs
34181	AA403298	Hs.81178	ESTs
23211	W68835	Hs.14159	Homo sapiens mRNA for KA0535 protein complete cds
40811	F46877	Hs.89275	EST
17291	AA173205	Hs.5101	Homo sapiens protein regulating cyclinase 1 (PRC1) mRNA complete cds
18712	N51752	Hs.42476	EST
30709	AA277963	Hs.27021	Homo sapiens semaphorin F homolog mRNA complete cds
1265	HQ4157-HT4427	Hs.26373	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds

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FIGURE 4 (CONT.)

1109	41	HC2261-IT3137	EST - J03261-IT3137	Hs 40123 Homo sapiens spleen micro checkpoint BUB3 (BUB3) mRNA complete cds
34367	42	A4351258	Hs 91504 ESTs	
34602	43	A4351468	Hs 32339 ESTs	
11565	44	A4452519	Hs 125014 ESTs	
8295	45	A4452582	Hs 11435 ESTs Weakly similar to SCF1 PROTEIN [Saccharomyces cerevisiae]	
17622	46	A4131584	Hs 61948 Human mRNA for KIAA0278 gene complete cds	
34754	47	A4287942	Hs 11085 ESTs Highly similar to G05 RIBOSOMAL PROTEIN L26 [Rattus norvegicus]	
31687	48	A4453116	Hs 141982 ESTs	
38622	49	A4589567	Hs 60756 CCK2B protein kinase 2	
25038	50	A4010065	Hs 80339 Collagen type I alpha 2	
32503	51	U17045	Hs 54749 SODIUM CHANNEL PROTEIN BRIAN II ALPHA SUBUNIT	
3478	52	A445325	Hs 80400 SODIUM CHANNEL PROTEIN BRIAN II ALPHA SUBUNIT	
3479	53	A445325	Hs 80400 SODIUM CHANNEL PROTEIN BRIAN II ALPHA SUBUNIT	
35087	54	A4453270	Hs 80400 ESTs	
31381	55	N87859	Hs 69337 ESTs	
26723	56	A4282781	Hs 95321 ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP23 [Saccharomyces cerevisiae]	
30584	57	A4459687	Hs 46024 ESTs	
38280	58	A4459687	Hs 120919 ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nucleobacter coarctans]	
14474	59	A4659427	Hs 24194 ESTs Moderately similar to RII ALU SUBFAMILY SC YAPING ENTRY III [H. sapiens]	
5312	60	U92718	Hs 79187 Human cell surface protein HCAR mRNA complete cds	
35588	61	A4461750	Hs 97343 EST	
29738	62	H99925	Hs 42770 EST	
7703	63	A4530094	EST - A4530096	
7703	64	A4530094	Hs 94403 ESTs	
32290	65	B11510	Hs 52954 ESTs	
9065	66	A314778	Hs 158494 ESTs Weakly similar to LITHOSTATHINE-1 BETA PRECURSOR [H. sapiens]	
224	67	D19633	Hs 77695 Human mRNA for KIAA0008 gene complete cds	
33658	68	W95477	Hs 50582 ESTs	
34065	69	A4195517	Hs 111650 ESTs Weakly similar to RII ALU SUBFAMILY J WARRING ENTRY III [H. sapiens]	
8028	70	X69503	Hs 00011 Adenylsuccinate synthase	
4106	71	U29483	Hs 106102 Cytochrome B501	
41099	72	H92368	Hs 81107 H. sapiens mRNA for Hsf1 protein	
8764	73	A4401334	Hs 109441 ESTs	
27588	74	A443197	Hs 41161 ESTs	
32052	75	A443197	Hs 125351 ESTs	
1931	76	A4320860	Hs 10328 Human beta-casein-like protein 1 (beta-casein) mRNA complete cds	
11078	77	A4193399	Hs 26841 ESTs	
35223	78	A4921348	Hs 110942 ESTs Highly similar to DOUCYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae]	
8771	79	A4911188	Hs 82273 ESTs	
7898	80	A4353032	Hs 81634 ESTs	
19902	81	H66726	Hs 34180 ESTs	
10716	82	A4033319	Hs 9951 ESTs	
13193	83	A4442783	Hs 20483 ESTs Highly similar to G2MITOTIC-SPECIFIC CYCLIN B2 [Mus musculus]	
9590	84	X17623	Hs 118538 NUCLEOSIDE DIPHOSPHATE KINASE A	
31735	85	A4193226	Hs 117828 ESTs	
31735	86	A4193226	Hs 117828 ESTs	
28231	87	D20981	Hs 82403 ESTs	
28248	88	A4537152	Hs 71969 ESTs	
33036	89	W46550	Hs 39572 ESTs Weakly similar to transcription LRE2 reverse transcriptase homolog [H. sapiens]	
28106	90	A4455984	Hs 110462 ESTs	
38690	91	A4500721	Hs 111467 ESTs	
20203	92	N28555	Hs 5556 ESTs Moderately similar to RII ALU SUBFAMILY SC WARRING ENTRY III [H. sapiens]	
10251	93	R78185	Hs 18171 ESTs Weakly similar to ODH67 [C. elegans]	
31536	94	R72680	Hs 57133 Natural resistance-associated macrophage protein 2	
1372	95		EST - K01884	

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FIGURE 4 (CONT.)

39242	AA421523	Hs.110032 ESTs	Hs.110032 ESTs
27354	AA425221	Hs.81008 ESTs	Hs.81008 ESTs
4332	U98189	Hs.78279 Human placenta (QF53) mRNA complete cds	Hs.78279 Human placenta (QF53) mRNA complete cds
10126	AA456020	Hs.110070 Human testis (QF53) mRNA partial cds	Hs.110070 Human testis (QF53) mRNA partial cds
42463	U98190	EST - RC_A008007	EST - RC_A008007
31795	U98190	Hs.100318 ESTs	Hs.100318 ESTs
27828	N80703	Hs.50473 ESTs	Hs.50473 ESTs
75240	AA039713	Hs.110406 ESTs	Hs.110406 ESTs
4341	U39545	Hs.82507 Human ARF-activated phosphatidylinositol-specific phospholipase D1a (p15L1) mRNA complete cds	Hs.82507 Human ARF-activated phosphatidylinositol-specific phospholipase D1a (p15L1) mRNA complete cds
17483	AA122147	Hs.84691 ESTs	Hs.84691 ESTs
3709	U07550	Hs.71622 ESTs	Hs.71622 ESTs
8068	U07550	Hs.11187 Head stock 10 KD protein 1 (chaperonin 10)	Hs.11187 Head stock 10 KD protein 1 (chaperonin 10)
40148	U07550	Hs.111250 KERATIN TYPE II CYTOSKELETAL 80	Hs.111250 KERATIN TYPE II CYTOSKELETAL 80
20418	AA46920	Hs.123175 ESTs	Hs.123175 ESTs
27695	AA470155	Hs.75307 Human RNA binding protein C1-3 mRNA complete cds	Hs.75307 Human RNA binding protein C1-3 mRNA complete cds
7971	AA481423	Hs.126399 ESTs	Hs.126399 ESTs
27809	AA481793	Hs.64761 ESTs	Hs.64761 ESTs
24677	Z39338	Hs.21201 ESTs	Hs.21201 ESTs
9278	D59418	Hs.33886 Homo sapiens importin-alpha homolog (SRP1) (genomic) mRNA complete cds	Hs.33886 Homo sapiens importin-alpha homolog (SRP1) (genomic) mRNA complete cds
17678	AA134275	Hs.134510 Human IIV1 late element modulatory factor mRNA sequence from chromosome 3	Hs.134510 Human IIV1 late element modulatory factor mRNA sequence from chromosome 3
36709	AA421205	Hs.13889 ESTs	Hs.13889 ESTs
20094	H99053	Hs.10508 ESTs	Hs.10508 ESTs
9713	L44338	Hs.78494 Homo sapiens mRNA for KIAA0225 protein partial cds	Hs.78494 Homo sapiens mRNA for KIAA0225 protein partial cds
28022	D11837	Hs.22848 ESTs	Hs.22848 ESTs
29044	AA148985	Hs.111740 ESTs	Hs.111740 ESTs
2492	M22868	Hs.18448 Tumor protein p53 (L1-Fragment syndrome)	Hs.18448 Tumor protein p53 (L1-Fragment syndrome)
14904	T83369	Hs.107147 ESTs	Hs.107147 ESTs
22075	AA043765	Hs.54648 H sapiens R1-1 mRNA for putative nucleic acid binding protein	Hs.54648 H sapiens R1-1 mRNA for putative nucleic acid binding protein
13606	AA459437	Hs.20386 ESTs	Hs.20386 ESTs
42007	T90585	EST - RC_T06355	EST - RC_T06355
1544	J05368	Hs.2012 TRANSCOBALANIN PRECURSOR	Hs.2012 TRANSCOBALANIN PRECURSOR
42311	T97237	Hs.84560 ESTs	Hs.84560 ESTs
40219	U34920	Hs.30253 INITIAL ONCE-ACTOR IF-2 MITOCHONDRIAL PRECURSOR	Hs.30253 INITIAL ONCE-ACTOR IF-2 MITOCHONDRIAL PRECURSOR
330797	U34920	Hs.30253 Human testis phosphatase (p19P-2) mRNA complete cds	Hs.30253 Human testis phosphatase (p19P-2) mRNA complete cds
17220	AA055070	Hs.3281 EST - RC_A0033070_3	Hs.3281 EST - RC_A0033070_3
24322	W83782	Hs.18328 ESTs	Hs.18328 ESTs
32587	AA412057	Hs.68117 ESTs	Hs.68117 ESTs
8338	AA417152	Hs.5101 Homo sapiens protein regulating cyclin111 (PRC1) mRNA complete cds	Hs.5101 Homo sapiens protein regulating cyclin111 (PRC1) mRNA complete cds
387	D25389	EST - D25389	EST - D25389
12319	AA398109	Hs.20990 ESTs	Hs.20990 ESTs
15643	W95247	Hs.27437 ESTs	Hs.27437 ESTs
12118	AA180488	Hs.33746 ESTs	Hs.33746 ESTs
18339	AA025206	Hs.1151 Human mRNA for KIAA0072 gene partial cds	Hs.1151 Human mRNA for KIAA0072 gene partial cds
12520	U72531	Hs.9771 ESTs	Hs.9771 ESTs
22595	AA413242	Hs.107092 H420103170	Hs.107092 H420103170
34018	AA191488	Hs.75614 Human high-affinity capote usefate protein (ICTR1) mRNA complete cds	Hs.75614 Human high-affinity capote usefate protein (ICTR1) mRNA complete cds
251	D14520	Hs.84728 Basic transcription element binding protein 2	Hs.84728 Basic transcription element binding protein 2
31778	U095448	Hs.303 Zinc finger protein 139 (zfp139)	Hs.303 Zinc finger protein 139 (zfp139)
24535	Z38409	Hs.8053 ESTs	Hs.8053 ESTs
18127	AA060699	Hs.35441 ESTs	Hs.35441 ESTs

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FIGURE 4 (CONT.)

26146	3.4	AA250824	Hs 60478	ESTs Weakly similar to ZINC FINGER PROTEIN 91 [H sapiens]
4011	3.4	U75535	Hs 3280	Human cysteine protease MO2 mRNA alpha (MO2) mRNA complete cds
5660	3.4	X15094	Hs 31721	NAADPH-DEPENDENT METHYLENE TETRAHYDROFOLATE DEHYDROGENASE
76270	3.4	AA242080	Hs 47222	ESTs
35227	3.4	AA242086	Hs 98395	ESTs
17176	3.4	AA101381	Hs 68300	CRABP-RELATED PROTEIN-RCCT
17263	3.4	AA101381	Hs 68300	ESTs
15098	3.3	W16684	Hs 74284	ESTs Moderately similar to Similar to 5 carboxylase hypodermal protein L3111 [H sapiens]
17675	3.3	AA134054	Hs 44016	ESTs
10009	3.3	N81193	Hs 43133	Human spleen mRNA for KIAA0628 protein complete cds
33885	3.3	AA181560	Hs 61890	Human spleen Impo1a beta subunit mRNA complete cds
9270	3.3	H85189	Hs 24937	Human spleen sodium/hydrogen exchanger (SLC5A3) gene complete cds
37351	3.3	AA458079	Hs 7256	ESTs
18367	3.3	AA224150	Hs 10332	ESTs Moderately similar to overexpression protein [H. norvegicus]
13130	3.3	AA588472	Hs 8739	ESTs Highly similar to HYPOHEMICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PMT&PCT INTERGENIC REGION [Saccharomyces cerevisiae]
18220	3.3	H12534	Hs 8104	ESTs
18469	3.3	AA458089	Hs 11907	ESTs
21551	3.3	R35073	Hs 24568	ESTs
13767	3.3	AA453234	Hs 11907	ESTs
4739	3.3	U53768	Hs 7501	Human FX protein mRNA complete cds
7258	3.3	AA075427	Hs 17798	ESTs
17041	3.3	AA070394	Hs 44131	ESTs
15504	3.3	W23362	Hs 86081	ESTs
18214	3.3	AA190635	Hs 35987	Human pre-mitochondrial factor alpha 3 p8 subunit mRNA complete cds
7401	3.3	AA066000	Hs 17215	Human spleen cDNA 23071 unknown mRNA partial cds
18912	3.3	U10713	Hs 10228	Human spleen mRNA for unknown protein complete cds
18917	3.3	AA458089	Hs 31748	Human spleen mRNA for TRES
9140	3.3	H26443	Hs 31748	Human spleen mRNA for TRES
2148	3.2	L41390	EST - L41390	EST - L41390
18883	3.2	F04258	Hs 36454	ESTs Highly similar to NORGANIC PYROPHOSPHATASE [Bos taurus]
33891	3.2	HUMTFRN1:1507	Hs 91379	AFK-HUMTFRN11507_M
15340	3.2	X76944	Hs 87157	TYBASSOCIATED SPLICING FACTOR
872439	3.2	K87439	Hs 9122	Human O6 protein mRNA partial cds
3256	3.2	U41387	Hs 21730	ESTs
4400	3.2	R15849	Hs 24297	ESTs
21350	3.2	AA280925	Hs 45793	ESTs Weakly similar to H14LU SUBFAMILY J WARNING ENTRY [H sapiens]
11881	3.2	H18557	Hs 45793	ESTs
22390	3.2	AA53228	Hs 45793	ESTs
14111	3.2	U10713	Hs 21043	ESTs
13454	3.2	AA453431	Hs 8047	ESTs
12908	3.1	AA427578	Hs 42179	ESTs
31309	3.1	N65818	Hs 54174	ESTs
31192	3.1	N64408	Hs 23916	ESTs
11258	3.1	AA195512	Hs 82962	Thymidylate synthase
172	3.1	D00356	Hs 48915	Human spleen serine/threonine kinase (STAK) mRNA complete cds
28105	3.1	AA243133	Hs 32708	Human spleen MAO3-like protein kinase mRNA complete cds
11059	3.1	AA251809	Hs 12338	ESTs
19177	3.1	H10934	Hs 10304	ESTs
7380	3.1	AA458089	Hs 10304	ESTs
42308	3.1	U42308	Hs 63320	ESTs Weakly similar to GABLING PROTEIN BE(A-2 CHN) [H sapiens]
18315	3.1	W95028	Hs 131801	PRYVAITE DEHYDROGENASE E1 COMPLEXENI ALPHA SUBUNIT TEST IS SPECIFIC FORM PREDHSCR
3109	3.1	N95028	Hs 48290	Human spleen mRNA for VRK1 complete cds
17499	3.1	AA112979	Hs 15140	ESTs
14130	3.1	AA488041	Hs 3266	ESTs Highly similar to phosphorylation regulatory protein p12 [H sapiens]
14134	3.1	AA488041	Hs 3266	ESTs Highly similar to T3C317 [C. elegans]
42421	3.1	W45491	Hs 108835	ESTs Weakly similar to T3C317 [C. elegans]
15723	3.1	W79260	Hs 5337	ESTs Highly similar to ribosome-binding protein p34 [H. norvegicus]

FIGURE 4 (CONT.)

11140	31	AA158132	Hs 11817 ESTs Highly similar to YSA1 PROTEIN (Sclerodermatopathy associated)
14322	31	AA158133	Hs 27893 ESTs Highly similar to PCBALE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C1E11 C2C (Schistosomiasis parasite)
17362	31	Z11400	Hs 30019 ESTs
17362	31	AA158134	Hs 15818 ESTs
22113	31	AA158135	Hs 15817 ESTs
33520	31	AA158136	Hs 48652 ESTs
17825	31	AA158137	Hs 31730 Homo sapiens RNA binding protein Gyr (GTY-48BP) mRNA complete cds
5053	31	U81992	Hs 71134 Human TGF- β 1 mRNA complete cds
15090	31	U84999	Hs 93121 Human LCN protein mRNA complete cds
17157	31	AA147224	Hs 71814 EST
28330	31	AA278050	Hs 73291 ESTs
22600	31	T10272	Hs 4327 ESTs
4789	31	U96448	Hs 74374 Human Cdz2-desiccation esterase protein for secretion mRNA complete cds
7445	31	AA104023	Hs 110048 ESTs
75355	31	AA178387	Hs 73396 ESTs
75355	31	AA178388	Hs 73397 ESTs
806	31	AA178389	Hs 73398 ESTs
38447	31	AA504255	Hs 94104 Human protein kinase A1P mRNA complete cds
41464	31	R48537	Hs 107450 ESTs
9097	31	L18181	Hs 121541 TRANSLOCATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT
13174	31	U87987	Hs 87246 Human Bcl-2 binding compound 3 (bbcl2) mRNA partial cds
33820	31	V93943	Hs 99509 ESTs
41077	31	N95025	Hs 126031 ESTs
1930	31	L24534	Hs 73039 Human (p23) mRNA complete cds
32159	31	U87988	Hs 99510 ESTs
32159	31	R47081	Hs 126032 ESTs
11839	31	AA159640	Hs 28991 ESTs
11839	31	AA281251	Hs 32690 ESTs Highly similar to tyrosine protein tyrosine phosphatase
6059	31	X58184	Hs 80810 Pesticidal human testis myocyte line HeCat mRNA 2100 nt
1605	31	L00053	Hs 79070 V-myc avian myeloblastosis viral oncogene homolog
4536	31	U43705	Hs 75502 Receptor protein-tyrosine kinase EDOB1
10173	31	R59878	Hs 102963 ESTs Highly similar to cell division control protein CDC21 (N. sapientis)
21009	31	N95401	Hs 28928 ESTs
38200	31	AA421164	Hs 107313 ESTs
32299	31	AA335022	Hs 73133 Transcription factor Ets 1 (microheterodimer transcription factor 1.4a)
8844	31	R47458	Hs 149963 Human SIC mRNA complete cds
10173	31	AA158138	Hs 73039 ESTs
5298	31	X52946	Hs 53108 MEEL-LIKE PROTEIN KINASE
18190	31	AA158139	Hs 53111 ESTs
18687	31	H61478	Hs 15841 ESTs
6081	31	X53398	Hs 82845 CD47 antigen (Rbc-related antigen integrin-associated signal transducer)
5254	31	U81822	Hs 10817 Human 26S proteasome-associated peptidomycin (POM1) mRNA complete cds
13579	31	AA453987	Hs 108705 Human neuronal PAS2 (NPAS2) mRNA complete cds
38495	31	AA505118	Hs 112255 Human nucleoside diphosphate (NDP) mRNA complete cds
2029	31	L33035	Hs 79808 RIBOSE 5-PHOSPHATE ISOMERASE
27374	31	AA435818	Hs 64641 ESTs Highly similar to YSCC12A 31C (elegans)
28128	31	AA435819	Hs 64642 ESTs
18708	31	U93238	Hs 32622 ESTs
357	31	AA435824	Hs 62853 ESTs
28045	31	U95156	Hs 79702 Human mRNA for transcriptional activator NSM2b complete cds
8059	31	AA252576	Hs 67287 ESTs
21358	31	AA310967	Hs 5080 ESTs Highly similar to TGA8.11 (C. elegans)
3572	31	R18079	Hs 14775 ESTs
11877	31	X53759	Hs 57764 Protein phosphatase 2C epsilon (human testis carcinoma mRNA 2346 nt)
35800	31	AA362327	Hs 9591 ESTs
	31	AA411448	Hs 136386 ESTs

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FIGURE 4 (CONT.)

2332	191715	Hs 14374	EST1 Highly similar to HYPOTHETICAL 103.6 NO PROTEIN IN COUS88 PH25 INTERGENIC REGION [Saccharomyces cerevisiae]
10961	AA126719	Hs 25382	EST1
26881	AA202659	Hs 03887	EST1
7199	AA215259	Hs 00800	Homo sapiens chromosome 19 contig t30703
11368	AA207114	Hs 27747	EST1
406	U74704	Hs 11178	Human anterior regulatory factor 1 mRNA complete cds
11819	AA204938	Hs 32471	EST1
11819	AA258189	Hs 32471	EST1
37433	AA454103	Hs 11001	EST1
5507	X13482	Hs 80508	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'
19841	H03617	Hs 5109	EST1 Highly similar to Ye407c-sp [S. cerevisiae]
12655	AA040882	Hs 10700	EST1
31574	H71303	Hs 50015	EST1
7814	AA107579	Hs 10268	EST1 Weakly similar to UBR1/UBINUCLEATING LIZIME E2-17 KO [Drosophila melanogaster]
7050	AA009913	Hs 10300	Homo sapiens epidermal de biosynthesis protease-2 (DPH2) mRNA complete cds
22319	W69900	Hs 19416	EST1
19070	H05970	Hs 13329	Human clone Z1607 mRNA sequence
17116	AA136369	Hs 14299	EST1
17116	AA136369	Hs 14299	EST1
8613	AA159455	Hs 31921	Homo sapiens mRNA for KIAA0649 protein partial cds
13965	AA108319	Hs 5307	EST1
39552	R03653	Hs 75374	PUTATIVE 60S RIBOSOMAL PROTEIN
1795	L13434	Hs 84162	Human chromosome 3p21.1 gene sequence complete cds
14746	D60354	Hs 90315	Human mRNA for KIAA0007 gene partial cds
2953	MA4929	Hs 75200	Protein phosphatase 2 (formerly 2A) regulatory subunit 8 (PR 52) alpha isoform
17899	AA420032	Hs 7487	EST1 Moderately similar to PTTQ gene product [R. norvegicus]
18003	AA171692	Hs 70940	EST1
42633	V02703	Hs 10239	EST1
1782	AA455296	Hs 10239	EST1
1782	AA455296	Hs 10239	EST1
8886	AA455296	Hs 10239	EST1
19437	AA214705	Hs 70371	EST1
27148	V07560	Hs 90718	EST1
32315	R05340	Hs 41729	Human lincRNA a splicing protein (HSP) mRNA complete cds
23210	AA048745	Hs 110457	EST1
9658	L10991	Hs 79009	Deoxythymidylase kinase
12210	AA293774	Hs 21261	EST1 Weakly similar to PROBABLE TRYPHOANYL-TRNA SYNTHETASE MITOCHONDRIAL [C. elegans]
33258	V02091	Hs 20330	Human mRNA for brainin-related protein partial cds
9652	L37747	Hs 09487	LAMIN B1
27862	AA455296	Hs 50653	EST1
1782	AA455296	Hs 50653	EST1
8886	AA455296	Hs 50653	EST1
5932	X07453	Hs 111449	EST1 Highly similar to HYPOTHETICAL 30.3.40 PROTEIN IN APE1A-AP4-CYP1 INTERGENIC REGION [Saccharomyces cerevisiae]
26824	AA287139	Hs 59348	EST1 Weakly similar to HYPOTHETICAL 30.3.40 PROTEIN IN APE1A-AP4-CYP1 INTERGENIC REGION [Saccharomyces cerevisiae]
5157	U80034	Hs 68585	Human mitochondrial intermedial peptide precursor (MPP) mRNA mitochondrial gene encoding mitochondrial protein complete cds
39434	AA497013	Hs 14292	EST1
7350	AA173505	Hs 35355	EST1
10960	U05337	Hs 09872	Human testis 50-repactive clone 1 (FAC1) mRNA complete cds
13385	AA455099	Hs 23151	EST1 Highly similar to NEUROLYSIN PRECURSOR [Rattus norvegicus]
33185	AA487509	Hs 03877	Homo sapiens mRNA for KIAA0088 protein complete cds
34078	AA281744	Hs 75810	Artemis XI (580D subcloning)
1474	AA281744	Hs 75810	Artemis XI (580D subcloning)
1474	AA281744	Hs 75810	Artemis XI (580D subcloning)
37420	AA226800	Hs 11314	EST1
16109	AA180681	Hs 58189	Homo sapiens neuroblastoma associated protein hEC mRNA complete cds
8463	X92098	Hs 75914	H sapiens mRNA for transmembrane protein mpc2.4
27444	AA430160	Hs 42785	EST1 Weakly similar to F25H9.7 [C. elegans]

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FIGURE 4 (CONT.)

30037	35	N27439	Hs 51632 EST	
27602	35	Hs 29635	EST, weakly similar to WDR12.7 [C. elegans]	
3390	35	S59184	Hs 79336 PRK, receptor like tyrosine kinase	
25042	35	A04010188	Hs 103035 EST	
40477	34	N24096	Hs 09246 Homo sapiens BAC clone TQ30622 from Tc21-c31.1	
18620	34	F27560	Hs 9417 EST	
15120	34	U73524	Hs 67465 Human putative A1P1 (P-binding protein) (HEAB) mRNA, complete cds	
26813	34	D59257	Hs 91181 Human C-1 mRNA, complete cds	
34723	34	A087115	Hs 06597 EST	
7993	34	A085277	Hs 80027 Homo sapiens brain expressed ring finger protein mRNA, complete cds	
18297	34	F11067	Hs 12344 EST	
25033	34	A085011	Hs 06597 EST	
452	34	D08076	Hs 24763 RAN binding protein 1	
11701	34	A053301	Hs 31730 Homo sapiens RRM RNA binding protein Gyr-1p (Gyr-1p) mRNA, complete cds	
1267	34	U83717	Hs 13055 EST	
42009	34	T83728	Hs 05821 Human osteoblast stimulating factor mRNA, complete cds	
28395	34	A0810064	EST - RC_133729	
36390	34	A0429291	Hs 73802 EST	
12916	34	A0427745	Hs 10657 EST, weakly similar to No definition line found [C. elegans]	
30766	34	A0435015	Hs 17965 Human C1-associated RS cytoplasmic CARD-Cys mRNA, complete cds	
14426	34	A060032	Hs 16077 EST	
14426	34	A060032	Hs 16077 EST, highly similar to AAC-RICH MINA CLONE AAC3 PROTEIN (Drosophila melanogaster)	
6307	34	A0429338	Hs 49541 EST	
11342	34	A0225874	Hs 105423 11 kDa protein for Sm protein F	
1497	34	J04068	Hs 14843 Homo sapiens mRNA for KIAA0704 protein in partial cds	
11454	34	A0333554	Hs 3378 Topoisomerase (DNA) II alpha (TOP2A)	
35976	34	W42788	Hs 1098 Human terminal deoxynucleotidyl transferase mRNA, complete cds	
27872	34	A0459234	Hs 48835 EST	
11823	34	A0433817	Hs 31055 EST	
11533	34	A0434607	Hs 16077 EST, highly similar to KIAA0659 protein, partial cds	
6231	34	X76131	Hs 28018 EST, highly similar to HYPOTHECIN, 402 KD PROTEIN K1314.3 IN CHROMOSOME II [Caenorhabditis elegans]	
24371	34	W87415	Hs 10911 EST, weakly similar to TIALU SUBFAMILY J WARNING ENTRY [H. sapiens]	
25286	34	A0452591	Hs 108259 EST	
8163	34	A0357294	Hs 08073 EST	
12233	34	A0343513	Hs 28813 EST, weakly similar to LINE1g H-chain fusion protein [M. musculus]	
14371	34	A0592216	Hs 30272 EST, moderately similar to ALR [H. sapiens]	
26169	34	A0251069	Hs 94576 EST, weakly similar to ORF YOR261c [S. cerevisiae]	
23005	34	T53339	Hs 7165 EST, highly similar to zinc finger protein [M. musculus]	
26594	34	N53955	Hs 13741 EST	
20837	34	N52553	Hs 20524 EST, highly similar to HEXOKINASE TYPE I [Homo sapiens]	
11145	34	N52553	Hs 08513 EST	
11375	34	A0448120	Hs 20203 Homo sapiens clone 2A708 mRNA, sequence	
17352	33	A030925	Hs 20980 EST	
11814	33	A0278607	Hs 24549 EST	
20796	33	D51272	EST - RC_D51272.9	
22491	33	R70012	Hs 29005 EST	
40847	33	N62354	Hs 109437 EST	
42022	33	T53138	Hs 19562 Homo sapiens mRNA for hTCF-4	
8053	33	A0309850	Hs 109527 EST	
363	33	O76528	Hs 123538 Human mRNA for RNA helicase, complete cds	
20796	33	A031123	Hs 4201 EST	
31855	33	N62354	Hs 109437 EST	
24092	33	W42943	Hs 14811 Homo sapiens protein tyrosine phosphatase PTP1 mRNA, complete cds	

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FIGURE 4 (CONT.)

[illegible]

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FIGURE 4 (CONT.)

41031	27	N91248	Hs.102897 ESTs	
24711	22	Z39645	Hs.21470 ESTs	
4733	22	U38538	Hs.57880 Human Lck-own protein mRNA with the p53 inter-1 complex cds	
29730	22	U93336	Hs.74860 ESTs	
34336	22	U93336	Hs.74860 ESTs	
1889	22	A4262802	Hs.104473 EST	
4118	22	U20591	Hs.1370 Adrenin II (depozitin III)	
20276	22	U20014	Hs.71122 IC12 PROTEASE PRECURSOR	
18238	22	U20919	Hs.27931 ESTs	
13250	22	AA466459	Hs.41145 ESTs	
34370	21	AA205352	Hs.27869 ESTs	
27898	21	AA351829	Hs.104038 ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MER-CR7 INTERGENIC REGION (Saccharomyces cerevisiae)	
18664	21	AA470156	Hs.60449 ESTs Weakly similar to dyenin 74K chain cyclase (R. norvegicus)	
34352	21	AA278955	Hs.18479 ESTs	
37415	21	AA278955	Hs.18479 ESTs	
14522	21	AA433807	Hs.9349 EST	
5173	21	AA433807	Hs.9349 EST	
10972	21	U81354	Hs.10050 ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION (Saccharomyces cerevisiae)	
22391	21	Hs.8359	Hs.5171 Homo septin signal recognition particle 72 (SRP72) mRNA complete cds	
40145	21	N52966	Hs.13284 ESTs	
3461	21	Hs.1391	Hs.81182 Human mRNA for histamine N-methyltransferase complete cds	
41893	21	U23811	Hs.51251 ESTs	
5807	21	AA45876	Hs.65058 Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN (EF-SSP-352) (H. sapiens)	
38155	21	AA45877	Hs.105980 ESTs	
824	21	HG1112-HT1112	Hs.105980 EST - HG1112-HT1112	
8384	21	AA424282	Hs.91728 Human T5-O autoantigen (TM-SC1) mRNA complete cds	
22185	21	AA227837	Hs.30705 Refinex polymerase 3 (K-linked receptor)	
24348	21	U68469	Hs.77899 Tropomyosin alpha chain (skeletal muscle)	
35340	21	AA398920	EST - RC_AA398920	
10888	21	AA112023	Hs.15313 ESTs Weakly similar to PRE-MIRNA SPLICING HELICASE BHR2 (S. cerevisiae)	
381	21	D28473	Hs.78770 Isomerase RNA synthetase	
27051	21	AA46044	Hs.31975 ESTs Weakly similar to TIT-ALL GLOB FAMILY JNMRING ENTRY (H. sapiens)	
11828	21	AA46044	Hs.31975 ESTs Weakly similar to TIT-ALL GLOB FAMILY JNMRING ENTRY (H. sapiens)	
5448	21	AA278323	Hs.7241 Homo sapiens clone 24009 mRNA sequence	
35956	21	U02751	Hs.69855 Neuroblastoma RAS viral (v-ras) oncogene homolog	
7525	21	AA142533	Hs.109571 ESTs	
35532	21	AA142538	Hs.69851 ESTs	
28229	21	F09351	Hs.18492 ESTs Weakly similar to weakly similar to S. cerevisiae PTM1 precursor (C. elegans)	
18423	21	AA178479	Hs.71992 ESTs	
33368	21	AA232103	Hs.53112 ESTs	
20590	21	U68814	Hs.47283 ESTs	
12907	21	AA27577	Hs.34227 ESTs	
22958	21	U10288	Hs.25502 ESTs	
14250	21	AA458808	Hs.18122 ESTs	
26529	21	AA458831	Hs.17121 ESTs sapiens mRNA for Cdc7-related kinase complete cds	
9881	21	AA113149	Hs.82481 EST	
18378	21	AA275994	Hs.2910 Homo sapiens (H. sapiens) mRNA complete cds	
38040	21	U02371	Hs.2910 Phosphotyrosine phosphatase 2	
4111	21	AA205538	Hs.63314 ESTs	
	21	AA481403	Hs.107213 ESTs	
	21	U28312	Hs.63550 Human histonechromatin protein H4/H4-gamma mRNA complete cds	

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FIGURE 4 (CONT.)

33876	21	W037446	Hs 41241	ESTs	
25968	21	A4234935	Hs 65002	ESTs	
24856	21	Z3931	Hs 12599	Human sequence GPCR, U. Urokinase-type plasminogen activator (uPA) mRNA	uPA
33330	21	A4431148	Hs 105137	ESTs	
33481	20	A4431149	Hs 105138	ESTs	
33481	20	A4431150	Hs 105139	ESTs	
33481	20	A4431151	Hs 105140	ESTs	
33481	20	A4431152	Hs 105141	ESTs	
33481	20	A4431153	Hs 105142	ESTs	
33481	20	A4431154	Hs 105143	ESTs	
33481	20	A4431155	Hs 105144	ESTs	
33481	20	A4431156	Hs 105145	ESTs	
33481	20	A4431157	Hs 105146	ESTs	
33481	20	A4431158	Hs 105147	ESTs	
33481	20	A4431159	Hs 105148	ESTs	
33481	20	A4431160	Hs 105149	ESTs	
33481	20	A4431161	Hs 105150	ESTs	
33481	20	A4431162	Hs 105151	ESTs	
33481	20	A4431163	Hs 105152	ESTs	
33481	20	A4431164	Hs 105153	ESTs	
33481	20	A4431165	Hs 105154	ESTs	
33481	20	A4431166	Hs 105155	ESTs	
33481	20	A4431167	Hs 105156	ESTs	
33481	20	A4431168	Hs 105157	ESTs	
33481	20	A4431169	Hs 105158	ESTs	
33481	20	A4431170	Hs 105159	ESTs	
33481	20	A4431171	Hs 105160	ESTs	
33481	20	A4431172	Hs 105161	ESTs	
33481	20	A4431173	Hs 105162	ESTs	
33481	20	A4431174	Hs 105163	ESTs	
33481	20	A4431175	Hs 105164	ESTs	
33481	20	A4431176	Hs 105165	ESTs	
33481	20	A4431177	Hs 105166	ESTs	
33481	20	A4431178	Hs 105167	ESTs	
33481	20	A4431179	Hs 105168	ESTs	
33481	20	A4431180	Hs 105169	ESTs	
33481	20	A4431181	Hs 105170	ESTs	
33481	20	A4431182	Hs 105171	ESTs	
33481	20	A4431183	Hs 105172	ESTs	
33481	20	A4431184	Hs 105173	ESTs	
33481	20	A4431185	Hs 105174	ESTs	
33481	20	A4431186	Hs 105175	ESTs	
33481	20	A4431187	Hs 105176	ESTs	
33481	20	A4431188	Hs 105177	ESTs	
33481	20	A4431189	Hs 105178	ESTs	
33481	20	A4431190	Hs 105179	ESTs	
33481	20	A4431191	Hs 105180	ESTs	
33481	20	A4431192	Hs 105181	ESTs	
33481	20	A4431193	Hs 105182	ESTs	
33481	20	A4431194	Hs 105183	ESTs	
33481	20	A4431195	Hs 105184	ESTs	
33481	20	A4431196	Hs 105185	ESTs	
33481	20	A4431197	Hs 105186	ESTs	
33481	20	A4431198	Hs 105187	ESTs	
33481	20	A4431199	Hs 105188	ESTs	
33481	20	A4431200	Hs 105189	ESTs	
33481	20	A4431201	Hs 105190	ESTs	
33481	20	A4431202	Hs 105191	ESTs	
33481	20	A4431203	Hs 105192	ESTs	
33481	20	A4431204	Hs 105193	ESTs	
33481	20	A4431205	Hs 105194	ESTs	
33481	20	A4431206	Hs 105195	ESTs	
33481	20	A4431207	Hs 105196	ESTs	
33481	20	A4431208	Hs 105197	ESTs	
33481	20	A4431209	Hs 105198	ESTs	
33481	20	A4431210	Hs 105199	ESTs	
33481	20	A4431211	Hs 105200	ESTs	
33481	20	A4431212	Hs 105201	ESTs	
33481	20	A4431213	Hs 105202	ESTs	
33481	20	A4431214	Hs 105203	ESTs	
33481	20	A4431215	Hs 105204	ESTs	
33481	20	A4431216	Hs 105205	ESTs	
33481	20	A4431217	Hs 105206	ESTs	
33481	20	A4431218	Hs 105207	ESTs	
33481	20	A4431219	Hs 105208	ESTs	
33481	20	A4431220	Hs 105209	ESTs	
33481	20	A4431221	Hs 105210	ESTs	
33481	20	A4431222	Hs 105211	ESTs	
33481	20	A4431223	Hs 105212	ESTs	
33481	20	A4431224	Hs 105213	ESTs	
33481	20	A4431225	Hs 105214	ESTs	
33481	20	A4431226	Hs 105215	ESTs	
33481	20	A4431227	Hs 105216	ESTs	
33481	20	A4431228	Hs 105217	ESTs	
33481	20	A4431229	Hs 105218	ESTs	
33481	20	A4431230	Hs 105219	ESTs	
33481	20	A4431231	Hs 105220	ESTs	
33481	20	A4431232	Hs 105221	ESTs	
33481	20	A4431233	Hs 105222	ESTs	
33481	20	A4431234	Hs 105223	ESTs	
33481	20	A4431235	Hs 105224	ESTs	
33481	20	A4431236	Hs 105225	ESTs	
33481	20	A4431237	Hs 105226	ESTs	
33481	20	A4431238	Hs 105227	ESTs	
33481	20	A4431239	Hs 105228	ESTs	
33481	20	A4431240	Hs 105229	ESTs	
33481	20	A4431241	Hs 105230	ESTs	
33481	20	A4431242	Hs 105231	ESTs	
33481	20	A4431243	Hs 105232	ESTs	
33481	20	A4431244	Hs 105233	ESTs	
33481	20	A4431245	Hs 105234	ESTs	
33481	20	A4431246	Hs 105235	ESTs	
33481	20	A4431247	Hs 105236	ESTs	
33481	20	A4431248	Hs 105237	ESTs	
33481	20	A4431249	Hs 105238	ESTs	
33481	20	A4431250	Hs 105239	ESTs	
33481	20	A4431251	Hs 105240	ESTs	
33481	20	A4431252	Hs 105241	ESTs	
33481	20	A4431253	Hs 105242	ESTs	
33481	20	A4431254	Hs 105243	ESTs	
33481	20	A4431255	Hs 105244	ESTs	
33481	20	A4431256	Hs 105245	ESTs	
33481	20	A4431257	Hs 105246	ESTs	
33481	20	A4431258	Hs 105247	ESTs	
33481	20	A4431259	Hs 105248	ESTs	
33481	20	A4431260	Hs 105249	ESTs	
33481	20	A4431261	Hs 105250	ESTs	
33481	20	A4431262	Hs 105251	ESTs	
33481	20	A4431263	Hs 105252	ESTs	
33481	20	A4431264	Hs 105253	ESTs	
33481	20	A4431265	Hs 105254	ESTs	
33481	20	A4431266	Hs 105255	ESTs	
33481	20	A4431267	Hs 105256	ESTs	
33481	20	A4431268	Hs 105257	ESTs	
33481	20	A4431269	Hs 105258	ESTs	
33481	20	A4431270	Hs 105259	ESTs	
33481	20	A4431271	Hs 105260	ESTs	
33481	20	A4431272	Hs 105261	ESTs	
33481	20	A4431273	Hs 105262	ESTs	
33481	20	A4431274	Hs 105263	ESTs	
33481	20	A4431275	Hs 105264	ESTs	
33481	20	A4431276	Hs 105265	ESTs	
33481	20	A4431277	Hs 105266	ESTs	
33481	20	A4431278	Hs 105267	ESTs	
33481	20	A4431279	Hs 105268	ESTs	
33481	20	A4431280	Hs 105269	ESTs	
33481	20	A4431281	Hs 105270	ESTs	
33481	20	A4431282	Hs 105271	ESTs	
33481	20	A4431283	Hs 105272	ESTs	
33481	20	A4431284	Hs 105273	ESTs	
33481	20	A4431285	Hs 105274	ESTs	
33481	20	A4431286	Hs 105275	ESTs	
33481	20	A4431287	Hs 105276	ESTs	
33481	20	A4431288	Hs 105277	ESTs	
33481	20	A4431289	Hs 105278	ESTs	
33481	20	A4431290	Hs 105279	ESTs	
33481	20	A4431291	Hs 105280	ESTs	
33481	20	A4431292	Hs 105281	ESTs	
33481	20	A4431293	Hs 105282	ESTs	
33481	20	A4431294	Hs 105283	ESTs	
33481	20	A4431295	Hs 105284	ESTs	
33481	20	A4431296	Hs 105285	ESTs	
33481	20	A4431297	Hs 105286	ESTs	
33481	20	A4431298	Hs 105287	ESTs	
33481	20	A4431299	Hs 105288	ESTs	
33481	20	A4431300	Hs 105289	ESTs	
33481	20	A4431301	Hs 105290	ESTs	
33481	20	A4431302	Hs 105291	ESTs	
33481	20	A4431303	Hs 105292	ESTs	
33481	20	A4431304	Hs 105293	ESTs	
33481	20	A4431305	Hs 105294	ESTs	
33481	20	A4431306	Hs 105295	ESTs	
33481	20	A4431307	Hs 105296	ESTs	
33481	20	A4431308	Hs 105297	ESTs	
33481	20	A4431309	Hs 105298	ESTs	
33481	20	A4431310	Hs 105299	ESTs	
33481	20	A4431311	Hs 105300	ESTs	
33481	20	A4431312	Hs 105301	ESTs	
33481	20	A4431313	Hs 105302	ESTs	
33481	20	A4431314	Hs 105303	ESTs	
33481	20	A4431315	Hs 105304	ESTs	
33481	20	A4431316	Hs 105305	ESTs	
33481	20	A4431317	Hs 105306	ESTs	
33481	20	A4431318	Hs 105307	ESTs	
33481	20	A4431319	Hs 105308	ESTs	
33481	20	A4431320	Hs 105309	ESTs	
33481	20	A4431321	Hs 105310	ESTs	
33481	20	A4431322	Hs 105311	ESTs	
33481	20	A4431323	Hs 105312	ESTs	
33481	20	A4431324	Hs 105313	ESTs	
33481	20	A4431325	Hs 105314	ESTs	
33481	20	A4431326	Hs 105315	ESTs	
33481	20	A4431327	Hs 105316	ESTs	
33481	20	A4431328	Hs 105317	ESTs	
33481	20	A4431329	Hs 105318	ESTs	
33481	20	A4431330	Hs 105319	ESTs	
33481	20	A4431331	Hs 105320	ESTs	
33481	20	A4431332	Hs 105321	ESTs	
33481	20	A4431333	Hs 105322	ESTs	
33481	20	A4431334	Hs 105323	ESTs	
33481	20	A4431335	Hs 105324	ESTs	
33481	20	A4431336	Hs 105325	ESTs	
33481	20	A4431337	Hs 105326	ESTs	
33481	20	A4431338	Hs 105327	ESTs	
33481	20	A4431339	Hs 105328	ESTs	
33481	20	A4431340	Hs 105329	ESTs	
33481	20	A4431341	Hs 105330	ESTs	
33481	20	A4431342	Hs 105331	ESTs	
33481	20	A4431343	Hs 105332	ESTs	
33481	20	A4431344	Hs 105333	ESTs	
33481	20	A4431345	Hs 105334	ESTs	
33481	20	A4431346	Hs 105335	ESTs	
33481	20	A4431347	Hs 105336	ESTs	
33481	20	A4431348	Hs 105337	ESTs	
33481	20	A4431349	Hs 105338	ESTs	
33481	20	A4431350	Hs 105339	ESTs	
33481	20	A4431351	Hs 105340	ESTs	

FIGURE 5

Primary Key	fold downregulated of Tumor vs	Accession	Unigene CLUSTER	Unigene Descriptor
2348	>10	M15656	Hs.75592	Adolase B fructose-bisphosphate
5463	>10	X90908	Hs.74126	H.sapiens mRNA for L-15P (L-BABP) protein
42133	>10	T73335	Hs.93184	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1583	>10	K02765	Hs.58512	COMPLEMENT C3 PRECURSOR
2426	>10	M18828	Hs.585	Apolipoprotein B (including Ag(x) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32966	H.sapiens mRNA for GCAP-III/uroguanylin precursor
1304	>10	U164310	EST - HG4310-HT4580	
5980	>10	X64559	Hs.65424	Tetranectin (plasminogen-binding protein)
41987	>10	T47089	Hs.121713	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24461	>10	W94427	Hs.3607	ESTs Weakly similar to SODIUMPOTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus
2372	>10	M15594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
15130	>10	U77643	Hs.95655	Human sapiens K12 protein precursor: mRNA complete cds
12467	>10	AA402656	Hs.28284	ESTs
41148	>10	R06984	Hs.50404	EST - RC_R06984_3
31652	>10	N73958	EST - U51010	Human chemokine (TECK) mRNA complete cds
4605	>10	U51010	ESTs	EST - U51010
28359	>10	AA609133	Hs.58115	ESTs
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
27108	>10	AA404397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
2848	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR
19537	>10	H30270	Hs.32583	ESTs
18784	>10	F09748	Hs.7974	ESTs
5773	>10	X54162	Hs.79386	64 KD AUTOANTIGEN D1

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FIGURE 5 (CONT.)

27387	>10	AA426330	Hs.78264	ESTs	
2886	>10	N59815	Hs.76882	Complement component 4A	
42530	>10	W72859	Hs.74569	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]	
827	>10	D87433	Hs.84753	Human mRNA for KIAA0246 gene partial cds	
550	>10	O78014	Hs.74568	Human mRNA for dihydropyrimidinase related protein-3 complete cds	
7026	>10	Z80345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain	
16736	>10	AA045306	Hs.42995	ESTs	
4630	>10	U52101	Hs.9699	Human YMP mRNA complete cds	
4655	>10	U52869	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19	
42758	>10	Z41411	Hs.107040	ESTs	
35537	>10	AA402533	Hs.29283	ESTs	
40392	>10	H95587	Hs.108890	ESTs	
7354	>10	AA092348	Hs.7858	ESTs	
9034	>10	C01833	Hs.29759	ESTs Weakly similar to IIII ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]	
10535	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]	
5520	>10	X06256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)	
2547	>10	M25609	Hs.10059	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 59/58kD isoform 1	
9003	>10	C00608	Hs.107882	ESTs	
41628	>10	R70212	Hs.79530	Immunoglobulin-associated alpha	
21934	>10	R44449	Hs.48778	ESTs	
11129	6	AA156873	Hs.15970	ESTs	
40387	7	H99460	Hs.108873	ESTs	

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FIGURE 6

Primary Key	Fold downregulated of Tumor	Accession	Unigene CLUSTER	Unigene Descriptor
2348	>10	M15656	Hs.75592	Aldolase B fructose-bisphosphate
6463	>10	X90908	Hs.74128	H.sapiens mRNA for I-15P (I-BABP) protein
42139	>10	T73335	Hs.83194	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1583	>10	K02785	Hs.58512	COMPLEMENT C3 PRECURSOR
2428	>10	M19828	Hs.595	Apelipoprotein B (including Ag(x) antigen)
8859	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38888	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32956	H.sapiens mRNA for GCAP-III/iguanylin precursor
1304	>10	HG4310-	Hs.65424	EST - HG4310-HT4580
5980	>10	X64559	Hs.121713	Tetranedrin (plasminogen-binding protein)
41887	>10	T47089	Hs.89552	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24451	>10	W94427	Hs.3807	ESTs Weakly similar to SODIUMPOTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus]
2372	>10	M16994	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89485	Glutathione S-transferase IV
1750	>10	U77643	Hs.95655	Carbonic anhydrase IV
15130	>10	AA402856	Hs.28264	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	R06984	ESTs	EST - RC_R06984_s
41148	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
31652	>10	T68873	Hs.143289	H.sapiens mRNA for metallothionein isoform 1R
23483	>10	U51010	EST - U51010	EST - U51010
4605	>10	AA609133	Hs.58115	ESTs
28359	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
24066	>10	W73194	Hs.80652	ESTs
33282	>10	AA284767	Hs.21910	ESTs
12084	>10	R48732	Hs.11006	ESTs
41473	>10	T29248	Hs.143113	Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds
32568	>10	X87159	Hs.37129	Sodium channel nonvoltage-gated 1 beta (Liddle syndrome)
6413	>10	NG4436	Hs.20813	ESTs
20707	>10	AA04397	Hs.58414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
27108	>10	AA403032	Hs.21701	ESTs
12477	>10	T61854	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
42059	>10	AA078072	Hs.1477	Insulin-like growth factor binding protein 6
25468	>10	AA303081	Hs.78293	ESTs
25910	>10			

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FIGURE 6 (CONT.)

16938	>10	AA059473	Hs.56783	ESTs	
41789	>10	T03735	Hs.26885	ESTs	
7754	>10	AA234634	Hs.76722	Human NF-IL6-beta protein mRNA complete cds	
8122	>10	X72012	Hs.75962	Endoglin (Osler-Rendu-Weber syndrome 1)	
2848	>10	M58286	Hs.150	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR	
23013	>10	T16661	Hs.6725	ESTs	
19537	>10	H30270	Hs.32583	ESTs	
4584	>10	U50350	Hs.32583	EST - U50350	
37410	>10	AA453652	Hs.59344	ESTs	
27969	>10	AA464594	Hs.63382	ESTs	
35497	>10	AA400606	Hs.144344	EST	
37013	>10	AA43690	Hs.136268	ESTs Highly similar to ZINC FINGER PROTEIN HF.12 (Homo sapiens)	
39247	>10	AA621553	Hs.112998	ESTs	
13471	>10	AA452598	Hs.109590	ESTs	
42110	>10	T88878	Hs.76688	Carboxylesterase 2 (liver)	
10965	>10	AA128997	Hs.18953	Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA complete cds	
4918	>10	U67733	Hs.3831	Human cGMP-stimulated 3',5'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA complete cds	
40737	>10	N54950	Hs.61454	H.sapiens KIK mRNA for katehexokinase clone pHKHK3a	
30403	>10	N45300	Hs.110647	Meis1 (mouse) homolog	
11432	>10	AA233389	Hs.361	ESTs	
18784	>10	F09748	Hs.7974	ESTs	
40662	>10	N49281	Hs.79386	EST - RC_N49281	
5773	>10	X54162	Hs.79386	84 KD AUTOANTIGEN D1	
35041	>10	AA350586	Hs.30862	ESTs	
20868	>10	N70068	Hs.7243	ESTs	
39729	>10	H11489	Hs.105805	ESTs	
27387	>10	AA426330	Hs.78264	ESTs	
39758	>10	I115814	Hs.80485	Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor) complete cds	
4319	>10	U37283	Hs.56882	Human microfilament-associated glycoprotein-2 MAGP-2 mRNA complete cds	
2866	>10	M59815	Hs.76582	Complement component 4A	
30332	>10	N39075	Hs.44934	EST	
41344	>10	R40189	Hs.6985	ESTs	
28271	>10	AA521200	Hs.48778	ESTs	
5634	>10	X57129	Hs.7644	HISTONE H1D	
19048	>10	H05464	Hs.100251	ESTs	
1479	>10	J02854	Hs.9515	Human 20-kDa myosin light chain (MLC-2) mRNA complete cds	
19401	>10	H27010	Hs.107384	ESTs	
29992	>10	N26386	Hs.33084	Solute carrier family 2 (facilitated glucose transporter) member 5	
2041	>10	L36033	Hs.77423	Stromal cell-derived factor 1	
22865	>10	R99909	Hs.36186	ESTs	

FIGURE 6 (CONT.)

11624	>10	AA243654	Hs.17998	ESTs	
12512	>10	AA405199	Hs.20733	ESTs	
41443	>10	R45577	Hs.10683	ESTs	
5055	>10	U77180	Hs.50002	Human mRNA for EBI1-ligand chemokine complete cds	
6038	>10	X08945	Hs.748	Basic fibroblast growth factor (bFGF) receptor (shorter form)	
42530	>10	W72859	Hs.74689	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]	
827	>10	D87433	Hs.84753	Human mRNA for KIAA0246 gene partial cds	
650	>10	D78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds	
37350	>10	AA452606	Hs.99289	EST	
37488	>10	AA455178	Hs.99397	ESTs	
36646	>10	AA431797	Hs.98783	EST	
38999	>10	AA609907		EST - RC_AA609907	
38191	>10	AA487895	Hs.17311	ESTs	
9944	>10	N57464	Hs.74670	Human mRNA for KIAA0146 gene partial cds	
8139	>10	AA341723	Hs.107374	ESTs	
41522	>10	R53966	Hs.75092	N-CHIMAERIN	
38090	>10	AA482603	Hs.111301	Mabk metalloproteinase 2 (gelatinase A 72kD gelatinase 72kD type IV collagenase)	
41175	>10	R09241		EST - RC_R09241	
36947	>10	AA437388	Hs.115726	ESTs	
4175	>10	U29953	Hs.76110	Pigment epithelium-derived factor	
35421	>10	AA399698	Hs.97669	EST	
4358	>10	U39487	Hs.250	Xanthine dehydrogenase	
35463	>10	AA400272	Hs.97758	EST	
7026	>10	Z80345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain	
34825	>10	AA282238	Hs.118463	Homo sapiens clone 24519 unknown mRNA partial cds	
20179	>10	N24879	Hs.9693	ESTs	
36805	>10	AA435901	Hs.55874	ESTs Weakly similar to p20 protein [R.norvegicus]	
24447	>10	W83121	Hs.23841	Human mRNA for KIAA0355 gene complete cds	
10247	>10	R74386	Hs.108924	ESTs	
3618	>10	U02388	Hs.101	Leukotriene B4 omega hydroxylase (cytochrome P450 subfamily IVF)	
1464	>10	J03474	Hs.3157	SERUM AMYLOID A PROTEIN PRECURSOR	
16842	>10	AA055163	Hs.57975	Homo sapiens mRNA for cardiac caldesmon complete cds	
16735	>10	AA045308	Hs.42598	ESTs	
22865	>10	R85880	Hs.33455	ESTs	
5248	>10	U86358	Hs.50404	Human chemokine (TECK) mRNA complete cds	
7510	>10	AA136353	Hs.38022	ESTs	
34683	>10	AA264920	Hs.13718	ESTs	
19885	>10	H86980	Hs.12112	ESTs Moderately similar to protein phosphatase 1 binding protein PTG [M.musculus]	
9959	>10	N75215	Hs.43148	ESTs	
38135	>10	AA468185	Hs.125176	ESTs	

FIGURE 6 (CONT.)

36702	>10	AA434108	Hs.101393	ESTs Moderately similar to DNAJ PROTEIN HOMOLOG 1 [Homo sapiens]
3357	>10	M99487	Hs.1915	PROSTATE-SPECIFIC MEMBRANE ANTIGEN
36783	>10	AA435805	Hs.112065	EST
4876	>10	U65061	Hs.2048	Protease serine 2 (trypsin 2)
41149	>10	R06986	Il.76497	ESTs
15925	>10	Y13492	Hs.78483	Homo sapiens mRNA for smoothelin
12944	>10	AA428258	Hs.8769	ESTs
9317	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
19331	>10	H17885	Hs.23213	ESTs
5032	>10	U74382	Hs.90357	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds
34239	>10	AA235009	Hs.32246	ESTs
32852	>10	W31906	Hs.118428	ESTs
6432	>10	X69096	Hs.94413	Transient receptor potential channel 1
37001	>10	AA443311	Hs.96968	ESTs
4630	>10	U52101	Hs.9999	Human YMP mRNA complete cds
19489	>10	H27852	Hs.28137	ESTs
23028	>10	T17215	Hs.5952	ESTs
35359	>10	AA399061	Hs.112961	ESTs Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens]
4655	>10	U52969	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19
26030	>10	AA235984	Hs.87469	ESTs
41340	>10	R40395	Hs.112125	Lectin-like cholesterol acyltransferase
14494	>10	AA609645	Hs.25632	ESTs Weakly similar to PNG gene [H.sapiens]
4453	>10	U43916	Hs.79368	Human epithelial membrane protein (CL-20) mRNA complete cds
42758	>10	Z41411	Hs.107040	ESTs
35637	>10	AA402933	Hs.23283	ESTs
40392	>10	H99587	Hs.108880	ESTs
19360	>10	H19204	Hs.130468	ESTs
5184	>10	U82169	Hs.87234	Human frizzled homolog (FZD3) mRNA complete cds
850	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
1555	>10	K03207	Hs.103972	Salivary proline-rich protein
15574	>10	W38778	Hs.28216	ESTs
8965	>10	C00125	Hs.24332	ESTs Weakly similar to deoxyribose-phosphate aldolase [C.elegans]
33965	>10	AA182845	Hs.139088	Homo sapiens FIP2 alternatively translated mRNA complete cds
7949	>10	AA283620	Hs.34856	ESTs
11670	>10	AA252191	Hs.25199	Homo sapiens PAC clone DJ130H16 from 22q12.1-qter
7354	>10	AA092348	Hs.7858	ESTs
39151	>10	AA419011	Hs.98744	ESTs
42136	>10	T72481	Hs.73849	Apolipoprotein C-III
289	>10	D16480	Hs.75860	Hydroxyacyl-Coenzym A dehydrogenase3-ketocryl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein) alpha subunit
41379	>10	R42233	Hs.106487	Homo sapiens mRNA for KIAA0873 protein partial cds

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FIGURE 6 (CONT.)

34764	>10	AA287870	Hs.890	Lymphotoxin-beta
24515	>10	Z38289	Hs.12701	ESTs
18652	>10	F03111	Hs.22505	ESTs
37815	>10	AA469952	Hs.97899	ESTs
9034	>10	C01833	Hs.29759	ESTs Weakly similar to III ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]
34605	>10	AA291522	Hs.97250	EST
12248	>10	AA348198	Hs.14829	Homo sapiens mRNA for GABA-BR1a (nCB1a) receptor
42153	>10	T77729	Hs.89890	Pyruvate carboxylase
27110	>10	AA404494	Hs.84112	CTP synthetase
28831	>10	D59722	Hs.82824	ESTs
6333	>10	X82494	Hs.2653	Fibulin 2
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]
27257	>10	AA418001	Hs.46148	ESTs Weakly similar to mitogen-activated kinase kinase 5 [H.sapiens]
3631	>10	U03090	Hs.290	Homo sapiens Ca2+-dependent phospholipase A2 mRNA complete cds
4752	>10	U96632	Hs.3847	Glycoprotein Ib (platelet) beta polypeptide
3766	>10	U09579	Hs.74994	CYCLIN-DEPENDENT KINASE INHIBITOR 1
4310	>10	U37055	Hs.76034	Macrophage stimulating 1 (hepatocyte growth factor-like)
26923	>10	AA342302	Hs.55036	ESTs
5520	>10	X06256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
16720	>10	AA044732	Hs.77208	ESTs
25336	>10	AA053405	Hs.101404	ESTs
2547	>10	M25809	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58kD isoform 1
9786	>10	M63509	Hs.73974	Glutathione S-transferase M2 (muscle)
5206	>10	U82979	Hs.67846	Human clone HM18 monocytic inhibitory receptor precursor mRNA complete cds
9377	>10	H12674	Hs.9396	ESTs
41960	>10	T33511	Hs.4844	ESTs
21911	>10	R43980	Hs.26320	ESTs
16225	>10	AA011305	Hs.10029	Calthepsin C
16071	>10	AA001426	Hs.40863	ESTs
29335	>10	H88239	Hs.39122	ESTs
34966	>10	AA344866	Hs.1285	Complement component 8 gamma polypeptide
21076	>10	N99976	Hs.8016	ESTs
4402	>10	U41518	Hs.74692	AQUAPORIN-CHIP
20423	>10	N49308	Hs.104938	ESTs
16575	>10	AA031948	Hs.57548	ESTs
28284	>10	AA521080	Hs.46765	ESTs
9003	>10	C00808	Hs.107882	ESTs
5632	>10	X15357	EST - X15357	
20852	>10	N69540	Hs.17713	ESTs
34585	>10	AA281002	Hs.40735	ESTs

FIGURE 6 (CONT.)

33690	>10	Z38607	Hs.62248	ESTs	
8904	>10	AF002256	Hs.86180	ESTs	Homo sapiens killer cell receptor (KIR103) mRNA allele ASD1 complete cds
3307	>10	M85808	Hs.89578	EST	BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT
39200	>10	AA621246	Hs.112956	EST	
24712	>10	Z39652	Hs.27457	ESTs	
2199	>10	L49169	Hs.75678	ESTs	Human GOS3 mRNA complete cds
38942	>10	AA609546	Hs.94970	ESTs	Human mRNA for KIAA0306 gene partial cds
41628	>10	R70212	Hs.79630	ESTs	Immunoglobulin-associated alpha
6834	>10	Z18954	Hs.29960	ESTs	S100 calcium-binding protein A5 (formerly S100D)
40582	>10	N33212	Hs.107197	ESTs	
37333	>10	AA452158	Hs.75122	ESTs	TRANSFORMING PROTEIN RHOB
3992	>10	U19713	Hs.76354	EST	Allograft inflammatory factor 1
38734	>10	AA608792	Hs.112591	EST	
37836	>10	AA470135	Hs.112238	ESTs	
10000	>10	N79874	Hs.7915	ESTs	
30658	>10	N51105	Hs.111223	ESTs	
17629	>10	AA431919	Hs.69009	ESTs	
38260	>10	AA423970	Hs.96378	ESTs	
24122	>10	W46947	Hs.41186	ESTs	
1066	>10	HG3705-		EST - HG3705-HT2801	
12380	>10	AA398633	Hs.24872	ESTs	
26025	>10	AA235874	Hs.86888	ESTs	PUTATIVE DNA BINDING PROTEIN A20
41104	>10	R01398		EST - RC_R01398	
33586	>10	W93015	Hs.73166	ESTs	Treacher Collins syndrome susceptibility protein
26379	>10	AA058893	Hs.111841	ESTs	Human adenyl cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds
17607	>10	AA180530	Hs.72447	ESTs	
36638	>10	AA436163	Hs.95851	ESTs	Homo sapiens Ptg12 (PIG12) mRNA complete cds
19524	>10	H29566	Hs.83468	ESTs	Homo sapiens clone 23579 mRNA sequence
21934	>10	R44449	Hs.48778	ESTs	
32456	>10	T15829	Hs.66264	ESTs	
15440	>10	W27301	Hs.111552	ESTs	ESTs Moderately similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA [Thermomomyspora curvata]
2807	>10	M55210	Hs.87428	ESTs	Laminin gamma 1 (formerly LAMB2)
34193	>10	AA232251	Hs.128630	ESTs	
14584	>10	AA621414	Hs.110903	ESTs	Homo sapiens transmembrane protein mRNA complete cds
38752	>10	AA608852	Hs.112503	EST	
5294	>10	U80085	Hs.79351	ESTs	Human hwo P-domain K+ channel TWIK-1 mRNA complete cds
84	>10	AF001359		EST - AF001359_J	
4856	>10	U65093	Hs.82071	ESTs	Human msg1-related gene 1 (msg1) mRNA complete cds
13974	>10	AA479299	Hs.21107	ESTs	
26151	>10	AA250836	Hs.108508	ESTs	

FIGURE 6 (CONT.)

5938	>10	X62535	Hs.74044	Diacylglycerol kinase alpha (80kD)
17717	>10	AA138541	Hs.71647	EST
12404	>10	AA400292	Hs.23786	ESTs
2407	>10	M18737	Hs.90708	GRANZYME A PRECURSOR
26620	10	AA280413	Hs.89843	Spleen focus forming virus (SFFV) proviral integration oncogene spl1
37675	10	AA460377	Hs.99816	ESTs
41827	10	T15445	Hs.99491	H.sapiens mRNA for F25R3.3 kinase like protein from C.elegans
82	10	AF000959	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
203	10	D12820	Hs.106242	CYTOKROME P450 IVF3
24159	10	W57862	Hs.21289	ESTs
5302	10	U90543	Hs.79041	Human butyrophilin (BTf-1) mRNA complete cds
2219	10	L75670	Hs.105610	Homo sapiens rcal7 mRNA complete cds
24392	10	W88588	Hs.58569	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds
36159	10	AA419279	Hs.82813	Colony-stimulating factor 1 (M-CSF)
20251	10	AA504512	Hs.76852	ESTs Weakly similar to ZK792.1 [C.elegans]
37592	10	AA458668	Hs.95898	ESTs
39519	9	F10640	Hs.12354	ESTs
8240	9	AA397841	Hs.108879	ESTs
10887	9	AA101632	Hs.22971	ESTs
37500	0	AA455474	Hs.100530	ESTs
42550	9	W92272	Hs.25601	Homo sapiens zinc-finger helixase (hZFh) mRNA complete cds
9011	9	C01394	Hs.108823	Homo sapiens clone 24818 mRNA sequence
3490	9	S77783	Hs.75643	Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds
36691	9	AA432381	Hs.67357	ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE [H.sapiens]
3478	9	S76992	Hs.104005	Vav 2 oncogene
42034	9	T56281	Hs.110440	Human metallothionein (MT)-I-F gene
11945	9	AA259064	Hs.10839	ESTs Weakly similar to unknown [S.cerevisiae]
19317	9	H17476	Hs.11615	ESTs Weakly similar to dual specificity phosphatase [H.sapiens]
42395	8	W42733	Hs.108870	ESTs
11425	8	AA233257	Hs.25511	Homo sapiens mRNA for Hic-5 partial cds
15310	8	W19098	Hs.7921	ESTs
36801	8	AA431337	Hs.98017	ESTs
13499	8	AA453458	Hs.7301	ESTs
37514	8	AA455914	Hs.1019	Parathyroid hormone receptor 1
5998	8	X65844	Hs.75083	HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2
33589	8	W93074	Hs.59342	ESTs
5901	8	X55448	Hs.3118	H.sapiens mRNA for 2.19 gene
11129	8	AA156873	Hs.15970	ESTs
31987	8	N94551	Hs.55060	ESTs
40438	8	N21684	Hs.80500	Human mRNA for KIAA0061 gene partial cds

FIGURE 6 (CONT.)

34471	8	AA258843	Hs.111378	ESTs	
25530	8	AA038834	Hs.83428	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	
39471	7	D60265	Hs.107894	ESTs	
25100	7	AA018428	Hs.103343	EST	
15915	7	Y08858	Hs.82577	Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34) hypothetical protein E	
19097	7	H08171	Hs.30842	ESTs	
35353	7	AA388862	Hs.97699	ESTs	
36822	7	AA435978	Hs.98852	EST	
35530	7	AA400893	Hs.41717	Human 3'5' cyclic nucleotide phosphodiesterase (HSPDE1A3A) mRNA complete cds	
3869	7	U14417	Hs.106185	Human Ral guanine nucleotide dissociation stimulator mRNA partial cds	
1979	7	L29339	Hs.1064	Solute carrier family 5 (sodium/glucose cotransporter) member 1	
26178	7	AA251153	Hs.27910	Homo sapiens centromere Nek2-associated protein 1 (C-NAP1) mRNA complete cds	
36428	7	AA427605	Hs.98551	Human cardiac myosin binding protein-C (MyBP-C) gene complete cds	
26333	7	AA256075	Hs.82280	Homo sapiens regulator of G protein signaling 10 mRNA complete cds	
40387	7	H99460	Hs.108873	ESTs	
27236	7	AA417037	Hs.67805	ESTs	
20083	7	H98979	Hs.28029	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR (Mus musculus)	
21561	7	R33245	Hs.23076	ESTs	
21223	7	R08175	Hs.110130	Homo sapiens chromosome 19 cosmid F22329	
13405	7	AA450118	Hs.25722	ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens]	
34845	7	AA293420	Hs.95464	ESTs Moderately similar to transcription enhancer factor TEF1 [H.sapiens]	
15059	7	U53831	Hs.85280	Human interferon regulatory factor 7 (humit7) mRNA complete cds	
1945	7	L25878	Hs.89849	Epoxide hydrolase 1 intronoma (kenobiotic)	
42848	7	W92150	Hs.79310	Human GAP SH3 binding protein mRNA complete cds	
20041	7	H97012	Hs.11050	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]	
7053	6	Z84721	Hs.75702	Hemoglobin alpha 1	
23843	6	T92561	Hs.110422	ESTs	
25815	6	AA149889	Hs.96200	ESTs Weakly similar to A-kinase anchor protein 95 AKAP95 [R.norvegicus]	
8473	6	AA437346	Hs.2967	SHB adaptor protein (a Src homology 2 protein)	
34618	6	AA282143	Hs.58094	H.sapiens mRNA for melanoma growth regulatory protein MIA	
11074	6	AA148983	Hs.29068	ESTs	
17533	6	AA127098	Hs.71057	EST	
28973	6	F04014	Hs.65596	ESTs	
17042	6	AA070397		EST - RC_AA070397	
15248	6	W01094	Hs.84628	ESTs	
2247	6	M10321	Hs.110802	VON WILLEBRAND FACTOR PRECURSOR	
30810	6	N53419	Hs.47646	ESTs	
13348	6	AA449267	Hs.17914	ESTs Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT [H.musculus]	
1789	6	L13258	Hs.936	Solute carrier family 17 (sodium phosphate) member 2	
16827	5	AA038779	Hs.61826	Homo sapiens clone 23928 mRNA sequence	

FIGURE 6 (CONT.)

27103	5	AA040282	Hs.63481	ESTs Weakly similar to kynurenine/alpha-aminoacidate aminotransferase [R.norvegicus]
12631	5	AA412293	Hs.21258	ESTs
11599	5	AA242829	Hs.7508	ESTs
9010	5	C01360	Hs.67384	Homo sapiens clone 23904 mRNA sequence
4660	5	U53225	Hs.75283	Sortilin nexin 1
5244	5	U85992	Hs.87197	Human clone IMAGE:35527 unknown protein mRNA partial cds
7953	5	AA284403	Hs.74750	Homo sapiens mRNA for KIA00554 protein partial cds
27617	5	AA448114	Hs.55409	ESTs
39480	5	D60419	Hs.81915	STATMIN
37528	5	AA456112	Hs.99410	ESTs
11858	5	AA462308	Hs.106385	ESTs
37294	5	AA450127	Hs.110571	ESTs Highly similar to MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118 [Mus musculus]
23201	5	T40552	Hs.8278	ESTs
26767	5	D45608	Hs.83792	Surfactant pulmonary-associated protein D
3151	4	M83652	Hs.53155	Properdin P factor complement
29196	4	H24456	Hs.85053	Homo sapiens clone 24440 mRNA sequence
12863	4	AA425782	Hs.27973	ESTs
42486	4	W68410	Hs.106857	Calbindin 2 (28KD calretinin)
23571	4	T80628	Hs.108169	ESTs
12376	4	AA395271	Hs.19610	ESTs
27894	4	AA460319	Hs.48469	ESTs
28935	4	AFX-		AFX-HUMGAPDH/M33197_M
4238	4	U33053	Hs.2499	Human lipid-activated protein kinase PRK1 mRNA complete cds
41844	4	T15833	Hs.100227	EST
20111	4	N21380	Hs.25497	Hsapiens mRNA for ROX protein
8316	4	AA410529	Hs.30732	ESTs
39794	4	H21819	Hs.14895	Homo sapiens clone 24590 mRNA sequence
1517	4	J04501	Hs.772	Glycogen synthase 1 (muscle)
9164	4	D38081	Hs.85887	Thromboxane A2 receptor
35027	4	AA349986	Hs.95937	ESTs
14158	4	AA480182	Hs.118598	ESTs
41950	4	T33137	Hs.7967	ESTs
34360	4	AA251547	Hs.104358	EST
6547	4	X95208	Hs.9588	Human mRNA for KIA00385 gene complete cds
20863	4	N93089	Hs.19167	ESTs
12734	4	AA419200	Hs.5737	ESTs
39497	4	D80154	Hs.56340	ESTs
1600	4	K03474		EST - K03474
27148	4	AA406231	Hs.100113	Human mRNA for KIA00381 gene partial cds
10763	4	AA057620	Hs.30807	ESTs

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FIGURE 6 (CONT.)

17007	4	AA069696	Hs.67317	ESTs	
13522	4	AA454115	Hs.6000	ESTs	
18444	4	AA232646	Hs.68051	ESTs	
27665	3	AA447759	Hs.134724	ESTs	
21382	3	R16806	Hs.60615	PROTEIN KINASE C-THETA TYPE	
2052	3	L36818	Hs.75339	Inositol polyphosphate phosphatase-like protein 1 (51C protein)	
9039	3	C02049	Hs.106291	ESTs	
34888	3	AA303078	Hs.94479	Human GT334 protein (GT334) gene mRNA complete cds	
11047	3	AA142849	Hs.22650	ESTs	
19451	3	H23747	Hs.31697	ESTs	
2822	3	M55621	Hs.117946	N-acetylglucosaminyltransferase I	
13928	3	AA479441	Hs.11590	ESTs	
12064	3	AA283948	Hs.11367	ESTs Weakly similar to KIAA0009 [H.sapiens]	
3836	3	U12707	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	
4528	3	U48251	Hs.75871	Homo sapiens protein kinase C-binding protein RACK7 mRNA partial cds	
42064	3	T63384	Hs.9225	ESTs Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parastichopus parvinensis]	
4596	3	U50743	Hs.19520	Sodium/potassium ATPase gamma subunit	
4914	3	U67611	EST - U67611		
20168	3	N24106	Hs.2799	Cartilage linking protein 1	
24281	3	W79773	Hs.18511	ESTs	
19634	3	H44866	Hs.31597	ESTs	
10989	3	AA132366	Hs.8023	Homo sapiens mRNA for SPOP	
6587	3	X97748	EST - X97748		
14066	3	AA487559	Hs.8135	ESTs	
13350	3	AA448297	Hs.8944	ESTs Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens]	
33930	3	AA169539	Hs.95870	ESTs	
34215	3	AA233855	Hs.104252	UTROPHIN	
22509	3	R71393	Hs.29190	ESTs	
20065	3	H98857	Hs.27291	ESTs	
31091	3	N63078	Hs.138746	EST	
2493	3	M22919	Hs.77385	MYOSIN LIGHT CHAIN ALKALI SMOOTH-MUSCLE ISOFORM	
28913	3	F01560	Hs.22583	ESTs Highly similar to co-repressor protein [M.musculus]	
14323	3	AA598575	Hs.12851	ESTs	
34914	3	AA338729	Hs.133056	ESTs	
14236	3	AA498691	Hs.5011	ESTs Weakly similar to The ha1237 gene product is related to S.pombe rad21 gene product. [H.sapiens]	
24594	3	Z38804	Hs.22555	ESTs Highly similar to OP10D BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus]	
22589	3	R79580	Hs.29874	ESTs	
22156	3	R52145	Hs.25894	ESTs	
16404	3	AA021284	Hs.60554	ESTs Moderately similar to sodium-calcium exchanger form 3 [R.norvegicus]	
29310	3	H68942	Hs.88729	ESTs	

FIGURE 6 (CONT.)

8758	3	M26393	Hs.127810	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
9808	2	M78462	Hs.89033	Probable transcription factor PML (alternative products)
19289	2	H16568	Hs.23748	ESTs
34031	2	AA192614	Hs.83577	Human LIM protein MLP mRNA complete cds
33299	2	W73700	Hs.73803	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
3276	2	M93718	Hs.76983	Nitric oxide synthase 3 (endothelial cell)
31704	2	N75055	Hs.14532	ESTs
10310	2	R87373	Hs.75429	ESTs
22386	2	R63695	Hs.1432	Protein kinase C substrate 80K-H
20938	2	N73968	Hs.37477	ESTs Weakly similar to No definition line found [C.elegans]
5935	2	X62466	Hs.108338	CDW52 antigen (CAMPATH-1 antigen)
41465	2	R49889	Hs.5280	ESTs Weakly similar to C0608.3 [C.elegans]
25403	2	AA068316	EST - RC_AA068316	
27865	2	AA464267	Hs.24912	Homo sapiens bicucullin-D (BICO) mRNA complete cds
40632	2	N45221	EST - RC_N45221	
15527	2	W28798	Hs.63260	Phosphodiesterase 6A cGMP-specific rod alpha
31672	2	N74335	Hs.91681	ESTs
964	2	HG1804	EST - HG1804-HT1829	
12439	2	AA401452	Hs.32060	ESTs
24223	2	W70158	Hs.29696	ESTs
21052	2	N93764	Hs.10175	ESTs Weakly similar to hypothetical protein [H.sapiens]
34140	2	AA215637	Hs.104186	ESTs
5130	2	U79288	Hs.85053	Homo sapiens clone 24440 mRNA sequence
30041	2	N27628	Hs.132744	Homo sapiens clone 24525 mRNA sequence
19202	2	H11509	Hs.22482	ESTs
41350	2	R40442	Hs.75652	Glutathione S-transferase M5
914	2	HG1019	EST - HG1019-HT1019	
31958	2	N93495	Hs.54960	ESTs
12014	2	AA281769	Hs.7214	Human Hpaat (HPAST) mRNA complete cds
39777	2	H18412	Hs.75253	Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA alternatively spliced partial cds
19147	2	H09751	Hs.117619	ESTs
11199	2	AA176446	Hs.10024	ESTs
6477	2	X91504	Hs.64904	Transcription factor COUP 2 (a.k.a. ARP1)
16336	2	AA018601	Hs.75849	EXTRACELLULAR SIGNAL-REGULATED KINASE 3
24058	2	W23709	Hs.109047	ESTs
26180	2	AA251230	Hs.112272	ESTs
37177	2	AA447988	Hs.7765	ESTs
41994	2	T47601	Hs.138805	ESTs
36532	2	AA429889	Hs.68882	Acrosin
1450	2	J03071	Hs.115352	Growth hormone 1

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FIGURE 6 (CONT.)

24819	2	Z40923	Hs.24812	ESTs	
6532	2	X95325	Hs.89491	DNA-BINDING PROTEIN A	
27085	2	AA402495	Hs.77978	ESTs	
20487	2	N52322	Hs.19978	ESTs	
724	2	D83703	Hs.30729	Peroxisomal biogenesis factor 6	
4132	2	U27655	Hs.82294	Human RGP3 mRNA complete cds	
13375	2	AA449716	Hs.5723	ESTs	
13988	2	AA480045	Hs.7934	ESTs	
22306	2	R59906	Hs.100530	ESTs	
23167	2	T33164	Hs.12840	Homo sapiens germline mRNA sequence	
11320	2	AA213667	Hs.22222	ESTs	
24608	2	Z38888	Hs.25048	ESTs	
13163	2	AA437225	Hs.22410	ESTs	
1139	2	HG3227-	EST - HG3227-HT3404		
35572	2	AA401489	EST - RC_AA401489		
6964	2	Z49105	Hs.137591	H.sapiens HD21 mRNA	
30963	2	N59373	Hs.26812	ESTs	
16164	2	AA007509	Hs.75395	Human mRNA for TPRD complete cds	
2174	2	L42811	Hs.111758	KERATIN TYPE II CYTOSKELETAL 8D	
38958	2	AA609707	Hs.112751	ESTs	
37919	2	AA478162	Hs.104865	ESTs	
28905	2	D81123	Hs.57475	ESTs	
3745	2	U09117	Hs.80776	Human phospholipase c delta 1 mRNA complete cds	
19545	2	H37834	Hs.32659	ESTs	
8416	2	AA428531	EST - AA428531		
17569	2	AA128926	EST - RC_AA128926		
19354	2	H18829	Hs.121515	ESTs	
7598	2	AA174195	Hs.3354	Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA complete cds	
25385	2	AA059099	Hs.109727	ESTs	
14176	2	AA480620	Hs.11809	ESTs	
29487	2	H85120	Hs.80881	N-ACETYLACTOSAMINE SYNTHASE	
10197	2	R64199	Hs.50785	Homo sapiens vesicle trafficking protein sec22b mRNA complete cds	
19488	2	H27675	Hs.25804	ESTs	
10568	2	AA029703	Hs.38574	ESTs	
30799	2	N53143	Hs.64001	ESTs	
9638	2	L07592	Hs.106415	Human peroxisome proliferator activator receptor mRNA complete cds	
27195	2	AA411473	Hs.65311	ESTs	
17438	2	AA115508	Hs.2780	Jun D proto-oncogene	
24532	2	AFEX-	AFEX-HSAC07X00351_M		
10944	2	AA125968	Hs.34769	ESTs Weakly similar to F35G12.9 [C.elegans]	

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FIGURE 6 (CONT.)

42324	2	T98199	Hs.142702	ESTs	
34756	2	AA287665	Hs.8245	ESTs	
12743	2	AA421050	Hs.24545	ESTs	
13676	2	AA459389	Hs.26350	Homo sapiens mRNA for tyrosyl sulfotransferase-2	
13009	2	AA430474	Hs.16468	ESTs	
7403	2	AA094921	Hs.79788	ESTs	
35689	2	AA404707	Hs.54865	ESTs	
17701	2	AA135941	Hs.71626	ESTs	
18713	2	F04686	Hs.21782	ESTs	
8314	2	AA410355	Hs.103081	ESTs Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]	
7990	2	AA291788	Hs.32822	ESTs Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]	
42791	2	AFEX-		AFEX-HUMGAPDH433197_M	
6893	1	Z30543	Hs.123123	H.sapiens mRNA for chloride channel (putative) 2139bp	
35607	1	AA402287	Hs.133475	ESTs Weakly similar to zinc finger protein [H.sapiens]	
9468	1	H46074	Hs.31562	ESTs	
29469	1	H82929		EST - RC_H82929	
18692	1	F04444	Hs.8217	ESTs	
35205	1	AA398181	Hs.97602	ESTs	
22184	1	R53520	Hs.102755	ESTs	
28815	1	D59287	Hs.56782	ESTs	
17813	1	AA151480	Hs.91202	ESTs	
24655	1	Z39191	Hs.27282	ESTs Weakly similar to Lph17p [S.cerevisiae]	
15611	1	W51743	Hs.35096	ESTs	
15700	1	W73859	Hs.78061	Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds	
38770	1	AA435753		EST - RC_AA435753	
32400	1	R97178	Hs.110783	ESTs	
10802	1	AA069425	Hs.20573	ESTs	
17593	1	AA129858		EST - RC_AA129858	
20266	1	N32118	Hs.107305	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]	
14447	1	AA609045	Hs.11759	ESTs	
12892	1	AA426521	Hs.18528	Homo sapiens mRNA for NA14 protein	
19738	1	H53059	Hs.15548	ESTs	
14471	1	AA609346	Hs.20102	ESTs	
5786	1	X55018	Hs.89975	Cholinergic receptor nicotinic delta polypeptide	
18441	1	AA232508	Hs.77480	ESTs	
10164	1	R54743	Hs.19400	ESTs Weakly similar to MITOTIC MAO2 PROTEIN [S.cerevisiae]	
8830	1	AB002319	Hs.8863	Human mRNA for KIAA0321 gene partial cds	
8632	1	AA477891	Hs.104476	ESTs	
35520	1	AA402493	Hs.10552	ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus]	
35401	1	AA399593	Hs.97682	EST	

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FIGURE 6 (CONT.)

10801	1	AA112307	Hs.25224	ESTs	
18548	1	H37501	Hs.32705	ESTs	
30282	1	Hs.82364	ESTs		
39087	1	AA620907	Hs.111591	ESTs	
37896	1	AA477463	Hs.77039	Ribosomal protein S28	
41552	1	R59352	Hs.101253	Human mRNA for KIAA0296 gene complete cds	
11467	1	AA234089	Hs.14593	ESTs	
8215	1	AA389873	Hs.84344	ESTs Weakly similar to No definition line found [C.elegans]	
15505	1	W28366	Hs.7252	Homo sapiens clone 24800 mRNA sequence	
9834	1	M62259	Hs.22554	Homo sapiens clone 24800 mRNA sequence	
9159	1	D31483	Hs.90062	Homo sapiens clone 23565 unknown mRNA partial cds	
42218	1	T86444	Hs.110095	ESTs	
15526	1	W28790	Hs.8124	ESTs	
17780	1	AA150182	Hs.42262	ESTs Weakly similar to HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans]	
9777	1	M57888	Hs.95946	GRANZYME H PRECURSOR	
15373	1	W26376	Hs.74563	THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR	
12076	1	AA284382	Hs.5448	ESTs Weakly similar to No definition line found [C.elegans]	
15391	1	W26651	Hs.15961	ESTs	
12905	1	AA427537	Hs.32419	ESTs	
39820	1	H24085	Hs.25443	ESTs	
13109	1	AA435698	Hs.7985	ESTs	
24249	1	W73069	Hs.12600	ESTs	
18514	1	AA027946	Hs.46608	ESTs	
16767	1	AA046650	Hs.40342	ESTs	
15381	1	W26498	Hs.107725	ESTs Weakly similar to LIS-1 protein [H.sapiens]	
11690	1	AA252762	Hs.31235	ESTs	
22999	1	T16510	Hs.6624	ESTs	
24480	1	Z38153	Hs.26921	ESTs	
24368	1	W87280	Hs.124800	ESTs	
22565	1	R77631	Hs.29126	ESTs	
15356	1	W26105	Hs.8981	ESTs	
22772	1	W61319	Hs.37482	ESTs Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]	
18434	1	R58922	Hs.26590	ESTs	
22692	1	AA024484	Hs.81199	ESTs	
38830	1	R88711	Hs.34183	ESTs	
42547	1	AA609189	Hs.116415	ESTs	
34885	1	W73946	EST - RC_W73946		
18445	1	AA302831	Hs.57732	Homo sapiens p38beta2 MAP kinase mRNA complete cds	
18070	1	AA232648	Hs.87068	ESTs	
		AA180352	Hs.72733	ESTs	

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FIGURE 6 (CONT.)

23923 1 T98407 Hs.17812 ESTg

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FIGURE 7

Primary Key	fold downregulated of Tumor vs	Accession	Unigene CLUSTER	Unigene Descriptor
2348	>10	M15658	Hs.75592	Aldolase B fructose-bisphosphate
6463	>10	X60908	Hs.74126	H.sapiens mRNA for I-15P (I-BABP) protein
42139	>10	T73335	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1983	>10	K02785	Hs.58512	COMPLEMENT C3 PRECURSOR
2426	>10	M18828	Hs.585	Apolipoprotein B (including Ag(x) antigen)
8659	>10	AB002351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z36688	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32968	H.sapiens mRNA for GCAP-II/uroguanylin precursor
1304	>10	HG4310-	EST - HG4310-HT4580	
5980	>10	X64559	Hs.65424	Tetranectin (plasminogen-binding protein)
41887	>10	T47089	Hs.121713	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24461	>10	W94427	Hs.3807	ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus]
2372	>10	M16584	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89485	Carbonic anhydrase IV
15130	>10	U77643	Hs.85655	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA026556	Hs.28264	ESTs
41148	>10	R06984	EST - RC_R06984_3	
31652	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
23483	>10	T68873	Hs.143289	H.sapiens mRNA for metallothionein isoform 1R
4605	>10	U51010	EST - U51010	
28359	>10	AA609133	Hs.58115	ESTs
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
32568	>10	T29248	Hs.143113	Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds
6413	>10	X87159	Hs.37129	Sodium channel nonvoltage-gated 1 beta (Liddle syndrome)
20707	>10	N84436	Hs.20813	ESTs
27108	>10	AA04397	Hs.59414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
12477	>10	AA403032	Hs.21701	ESTs
42059	>10	T61654	Hs.93104	APOLIPOPROTEIN A-I PRECURSOR
25488	>10	AA079072	Hs.1477	Insulin-like growth factor binding protein 6
26910	>10	AA303081	Hs.78293	ESTs

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FIGURE 7 (CONT.)

16938	>10	AA058473	Hs.68783	ESTs	
41788	>10	T03735	Hs.25885	ESTs	
7754	>10	AA234634	Hs.76722	Human NF-IL6-beta protein mRNA complete cds	
6122	>10	X72012	Hs.75962	Endoglin (Osler-Rendu-Weber syndrome 1)	
2048	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR	
23013	>10	T16661	Hs.6725	ESTs	
19537	>10	H30270	Hs.32583	ESTs	
4584	>10	U50360	EST - U50360		
37410	>10	AA453652	Hs.93344	ESTs	
27969	>10	AA464594	Hs.63382	ESTs	
35497	>10	AA400608	Hs.144344	EST	
37013	>10	AA443650	Hs.138268	ESTs Highly similar to ZINC FINGER PROTEIN HF.12 (Homo sapiens)	
39247	>10	AA21553	Hs.112998	ESTs	
13471	>10	AA452598	Hs.105590	ESTs	
42110	>10	T68878	Hs.76688	Carboxylesterase 2 (liver)	
10955	>10	AA128997	Hs.18953	Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA complete cds	
4918	>10	U67733	Hs.3831	Human cGMP-stimulated 3',5'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA complete cds	
40737	>10	N54950	Hs.81454	H. sapiens KHK mRNA for ketohexokinase clone plIKHK3a	
30403	>10	N45300	Hs.110647	Meis1 (mouse) homolog	
11432	>10	AA233369	Hs.361	ESTs	
18784	>10	F03748	Hs.7974	ESTs	
40662	>10	N49281	EST - RC_N49281		
5773	>10	X54162	Hs.79386	64 KD AUTOANTIGEN D1	
35041	>10	AA350586	Hs.30862	ESTs	
20868	>10	N70068	Hs.7243	ESTs	
39729	>10	H11489	Hs.105805	ESTs	
27387	>10	AA426330	Hs.78284	ESTs	
39758	>10	H15814	Hs.80485	Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor) complete cds	
4319	>10	U37283	Hs.58882	Human microfibril-associated glycoprotein-2 MAGP-2 mRNA complete cds	
2866	>10	M59815	Hs.76682	Complement component 4A	
30332	>10	N39075	Hs.44934	EST	
41344	>10	R40189	Hs.6985	ESTs	
28271	>10	AA521200	Hs.48778	ESTs	
5034	>10	X57129	Hs.7644	HISTONE H1D	
10048	>10	H05464	Hs.100251	ESTs	
1429	>10	J02854	Hs.9515	Human 20-kDa myosin light chain (MLC-2) mRNA complete cds	
19491	>10	H27910	Hs.107384	ESTs	
29992	>10	N26386	Hs.33084	Solute carrier family 2 (facilitated glucose transporter) member 5	
2041	>10	L36033	Hs.77423	Stromal cell-derived factor 1	
27865	>10	R09809	Hs.36186	ESTs	

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FIGURE 7 (CONT.)

11624	AA243654	Hs.17898	ESTs
12512	AA405199	Hs.20733	ESTs
41443	R45577	Hs.10683	ESTs
5055	U77180	Hs.50002	Human mRNA for EBI1-ligand chemokine complete cds
6038	X68945	Hs.748	Basic fibroblast growth factor (bFGF) receptor (shorter form)
42530	W72859	Hs.74669	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]
827	D87433	Hs.84753	Human mRNA for KIAA0246 gene partial cds
850	D78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds
37350	AA452806	Hs.99289	EST
37488	AA455178	Hs.99397	ESTs
38646	AA431797	Hs.98763	EST
38998	AA609907		EST - RC_AA609907
38191	AA487895	Hs.17311	ESTs
9944	N57464	Hs.74670	Human mRNA for KIAA0148 gene partial cds
8138	AA341723	Hs.107374	ESTs
41522	R53966	Hs.75092	N-CHIMAERIN
38090	AA482603	Hs.111301	Matrix metalloproteinase 2 (gelatinase A 72kD gelatinase 72kD type IV collagenase)
41175	R09241		EST - RC_R09241
36947	AA437388	Hs.115728	ESTs
4175	U29953	Hs.76110	Pigment epithelium-derived factor
35421	AA389688	Hs.97659	EST
4358	U39487	Hs.250	Xanthine dehydrogenase
35463	AA400272	Hs.97758	EST
7028	Z80345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
34625	AA282238	Hs.118483	Human sapiens clone 24518 unknown mRNA partial cds
20179	N24879	Hs.9683	ESTs
36805	AA435901	Hs.56874	ESTs Weakly similar to p20 protein [R.norvegicus]
24447	W83121	Hs.23841	Human mRNA for KIAA0355 gene complete cds
10247	R74386	Hs.108924	ESTs
3618	U02398	Hs.101	Leukotriene B4 omega hydroxylase (cytochrome P450 subfamily IVF)
18730	F08876	Hs.8008	ESTs
22529	R73075	Hs.28327	EST
37520	AA455960	Hs.99405	ESTs
41122	R05483	Hs.138500	ESTs
4417	U42031	Hs.7557	Human 54 kDa progesterone receptor-associated immunophilin FKBP54 mRNA partial cds
9742	M14777	Hs.89552	Glutathione S-transferase A2
36194	AA421142	Hs.104672	ESTs
4445	U43653	Hs.3261	Leptin (murine obesity homolog)
19749	H53728	Hs.36608	ESTs
19763	H56965	Hs.34564	ESTs

FIGURE 7 (CONT.)

12713	>10	AA418398	Hs.17778	ESTs	SERUM AMYLOID A PROTEIN PRECURSOR
1464	>10	J03474	Hs.3157	ESTs	Homo sapiens mRNA for cardiac caldesmon complete cds
16842	>10	AA055163	Hs.57875	ESTs	
34229	>10	AA234383	Hs.3576	ESTs	
35563	>10	AA401404	Hs.112087	ESTs	
16736	>10	AA045306	Hs.42996	ESTs	
33607	>10	W93487	Hs.59488	ESTs	
16146	>10	AA005236	Hs.60162	ESTs	
22668	>10	R85890	Hs.33455	ESTs	
22562	>10	R77493	Hs.29653	EST	
22985	>10	T16211	Hs.6326	EST	Homo sapiens clone 23789 and 23825 mRNA sequence
5248	>10	U86358	Hs.50404	ESTs	Human clemokine (TECK) mRNA complete cds
27608	>10	AA443800	Hs.43125	ESTs	
7510	>10	AA136353	Hs.38022	ESTs	
34683	>10	AA284920	Hs.13718	ESTs	
27633	>10	AA446659	Hs.2563	ESTs	Tachykinin 2 (substance K neurokinin A neurokinin 2 neurokinin L neurokinin alpha neuropeptide K neuropeptide gamma)
32485	>10	T16335	Hs.65325	EST	
30791	>10	AA609018	Hs.112629	ESTs	
32020	>10	N95796	Hs.55181	ESTs	
19686	>10	H89980	Hs.12112	ESTs	Moderately similar to protein phosphatase 1 binding protein PTC [M. musculus]
30748	>10	N52254	Hs.47438	ESTs	
8903	>10	AF002246	Hs.21226	ESTs	Homo sapiens neural cell adhesion molecule (CALL) mRNA complete cds
9959	>10	N75215	Hs.43148	ESTs	
38138	>10	AA486185	Hs.125176	ESTs	
19845	>10	H59887	Hs.35187	ESTs	
1127	>10	HG3117-	HG3117-HT3293	EST	
23937	>10	T85315	Hs.15903	ESTs	
16599	>10	AA043349	Hs.62630	ESTs	
36702	>10	AA434108	Hs.101393	ESTs	Moderately similar to DNAX PROTEIN HOMOLOG 1 [Homo sapiens]
28930	>10	F02702	Hs.141503	ESTs	Small inducible cytokine A5 (RANTES)
9228	>10	D62584	Hs.109439	ESTs	Highly similar to OSTEOINDUCTIVE FACTOR PRECURSOR [Des launus]
3357	>10	M99487	Hs.1915	ESTs	PROSTATE-SPECIFIC MEMBRANE ANTIGEN
36763	>10	AA435805	Hs.112065	EST	
4876	>10	U66081	Hs.2048	ESTs	Protease serpin 2 (trypsin 2)
41149	>10	R06886	Hs.78487	ESTs	
22200	>10	RS4179	Hs.26100	ESTs	
15925	>10	Y13492	Hs.78483	ESTs	Homo sapiens mRNA for smoothelin
10911	>10	AA113387	Hs.24305	ESTs	
3336	>10	M97675	Hs.1944	ESTs	Human protein tyrosine kinase L-Ror1 (Ror1) mRNA complete cds
31889	>10	N91897	Hs.50652	ESTs	

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FIGURE 7 (CONT.)

10406	>10	AA007629	Hs.25478	ESTs	Integrin beta 2 (antigen CD18 (p85) lymphocyte function-associated antigen 1 macrophage antigen 1 (mac-1) beta subunit)
17737	>10	AA142875	Hs.71719	ESTs	
38939	>10	AA609632	Hs.112737	EST	
16206	>10	AA010611	Hs.80418	EST	
32810	>10	W15376	Hs.122656	ESTs	
18210	>10	AA196306	Hs.86045	ESTs	
24054	>10	W15580	Hs.15342	ESTs	
23047	>10	T23457	Hs.7120	ESTs	
12944	>10	AA428258	Hs.8769	ESTs	
34172	>10	AA227469	Hs.139171	EST	Human mRNA for KIAA0278 gene partial cds
9317	>10	D87488	Hs.40888	ESTs	
19331	>10	H17865	Hs.23213	ESTs	
21035	>10	N92824	Hs.14898	ESTs	
34208	>10	AA233380	Hs.104249	EST	
5974	>10	X64072	Hs.83968	ESTs	
5032	>10	U74382	Hs.90357	ESTs	
41941	>10	T32561	Hs.5476	ESTs	
34239	>10	AA235009	Hs.32248	ESTs	
32852	>10	W31906	Hs.116428	ESTs	
7662	>10	AA203527	Hs.18747	ESTs	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds
6432	>10	X89066	Hs.94413	ESTs	
37001	>10	AA443311	Hs.98998	ESTs	Transient receptor potential channel 1
4630	>10	U52101	Hs.9859	ESTs	Human YMP mRNA complete cds
19489	>10	H27852	Hs.28137	ESTs	
28483	>10	C14270	Hs.66357	ESTs	
19801	>10	H57357	Hs.18787	ESTs	Weakly similar to unknown protein [H.sapiens]
24672	>10	Z39300	Hs.124952	ESTs	
31153	>10	N63888	EST - RC_N63888	ESTs	
40250	>10	H82451	Hs.110	ESTs	Solute carrier family 3 (cystine dibasic and neutral amino acid transporters activator of cystine dibasic and neutral amino acid transport) member 1
23028	>10	T17215	Hs.6952	ESTs	
28072	>10	AA480886	Hs.55693	ESTs	
11868	>10	AA262556	Hs.28802	ESTs	Weakly similar to cerataurin alpha [R.norvegicus]
35359	>10	AA399061	Hs.112961	ESTs	Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens]
4285	>10	I155130	Hs.50130	ESTs	Human NECN related protein mRNA complete cds
4855	>10	U52999	Hs.80296	ESTs	BRAIN SPECIFIC POLYPEPTIDE PEP-19
26030	>10	AA235984	Hs.87469	ESTs	
2042	>10	L36051	Hs.1166	ESTs	Thrombopoietin (myeloproliferative leukemia virus oncogene ligand megakaryocyte growth and development factor)
25262	>10	AA045501	Hs.30250	ESTs	Homo sapiens short form transcription factor C-MAF (c-maf) mRNA complete cds
34821	>10	AA291983	Hs.144599	ESTs	
42405	>10	W44652	Hs.109898	ESTs	

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FIGURE 7 (CONT.)

41348	R40395	Hs.112125	Lecithin:cholesterol acyltransferase
14494	AA609645	Hs.25632	ESTs Weakly similar to PNG gene [H.sapiens]
4453	U43916	Hs.79368	Human epithelial membrane protein (CL-20) mRNA complete cds
42758	Z41411	ESTs	
2098	L39009	EST - L39009	
35637	AA402933	Hs.29283	ESTs
16549	AA029697	Hs.94854	ESTs
1220	HG3733-	EST - HG3733-HT4003	
39634	H52185	Hs.124994	ESTs
7735	AA232121	Hs.109631	Human tyrosyl-L-tryptophan synthetase mRNA complete cds
40392	H99587	Hs.108980	ESTs
37170	AA447779	Hs.99145	EST
18361	AA223502	Hs.86899	ESTs
19365	H19204	Hs.133466	ESTs
38429	AA498965	Hs.108694	Glycophorin A
38021	AA481059	Hs.105152	ESTs
5184	U92109	Hs.87234	Human frizzled homolog (FZD3) mRNA complete cds
27863	AA458923	Hs.70202	ESTs Weakly similar to F23B2.4 [C.elegans]
37476	AA455051	Hs.99386	EST
859	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
27185	AA410895	Hs.62348	ESTs
41010	N80598	Hs.21639	Human APEG-1 mRNA complete cds
38241	AA488076	Hs.105101	ESTs
22701	R89477	Hs.34299	ESTs
12152	AA291271	Hs.10896	ESTs Weakly similar to uroporphyrinogen III synthase UROIII [H.sapiens]
36913	AA609531	Hs.112050	ESTs
34034	AA192871	Hs.83760	Troponin I (skeletal fast)
37844	AA459857	Hs.99503	EST
4173	U29725	Hs.3080	Human BMK1 alpha kinase mRNA complete cds
16178	AA009839	Hs.1632	CD27L RECEPTOR PRECURSOR
20527	N54161	Hs.124044	ESTs
41918	T25873	Hs.102243	ESTs
1525	J04621	Hs.1501	Syndecan 2 (heparan sulfate proteoglycan 1 cell surface-associated fibroglycan)
19160	H10208	Hs.30972	EST
18860	AA059633	Hs.58152	ESTs Weakly similar to Ntsu [M.musculus]
36927	AA437259	Hs.104944	EST
1595	K03207	Hs.103972	Salivary proline-rich protein
15574	W38778	Hs.26216	ESTs
8985	C00125	ESTs Weakly similar to similar to deoxyribose-phosphate aldolase [C.elegans]	
33995	AA182845	Hs.139088	Homo sapiens FIP2 alternatively translated mRNA complete cds

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FIGURE 7 (CONT.)

7949	>10	AA283620	Hs.34956	ESTs	
16607	>10	AA034918	Hs.85079	ESTs	
11670	>10	AA252191	Hs.25199	Homo sapiens PAC clone DU130H16 from 22q12.1-qter	
7354	>10	AA092348	Hs.7858	ESTs	
4277	>10	U34879	Hs.85279	ESTRADIOL 17 BETA-DEHYDROGENASE 1	
23214	>10	T40855	Hs.11907	Human protein tyrosine phosphatase PTPCAAX1 (pPTPCAAX1) mRNA complete cds	
22209	>10	R54594	Hs.25209	ESTs	
38151	>10	AA419011	Hs.96744	ESTs	
23372	>10	T59537	EST - RC_T59537		
42138	>10	T72491	Hs.73849	Apolipoprotein C-III	
289	>10	D16480	Hs.75860	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/Coenzyme A hydratase (thiolase protein) alpha subunit	
15974	>10	Z36531	Hs.2859	H.sapiens mRNA for fibrinogen-like protein (pT49 protein)	
41379	>10	R42233	Hs.106487	Homo sapiens mRNA for KIAA0873 protein partial cds	
34764	>10	AA287870	Hs.590	Lymphotxin-beta	
24027	>10	W01875	Hs.5734	Homo sapiens mRNA for KIAA0879 protein partial cds	
36197	>10	AA421158	Hs.97514	ESTs	
37211	>10	AA448334	EST - RC_AA448334		
27684	>10	AA448625	Hs.57929	ESTs	
31790	>10	N80278	Hs.50891	ESTs	
24515	>10	Z36289	Hs.12701	ESTs	
18652	>10	F03111	Hs.22505	ESTs	
16535	>10	AA037433	Hs.46987	ESTs	
37815	>10	AA469952	Hs.97899	ESTs	
6364	>10	X03957	Hs.495	Prostaglandin E receptor 3 (subtype EP3) (alternative products)	
9034	>10	C01833	Hs.29759	ESTs Weakly similar to III ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]	
16489	>10	AA025728	Hs.61307	ESTs	
27034	>10	AA400102	Hs.49051	ESTs	
42746	>10	Z40646	Hs.124953	ESTs	
35368	>10	AA399269	Hs.15250	Homo sapiens DBI-related protein mRNA complete cds	
34805	>10	AA291522	Hs.97250	EST	
19983	>10	H89355	Hs.6598	ESTs	
31126	>10	N83444	Hs.47568	ESTs	
22516	>10	R81940	Hs.124964	ESTs	
12246	>10	AA348198	Hs.14829	Homo sapiens mRNA for GABA-BR1a (GGB1a) receptor	
8777	>10	AA495865	Hs.7874	ESTs	
13488	>10	AA453034	Hs.21041	ESTs Highly similar to FIBROPELIN C PRECURSOR (Strongylocentrotus purpuratus)	
25512	>10	AA085721	Hs.95511	ESTs	
29073	>10	F12567	EST - RC_F12567		
5541	>10	X01203	Hs.89751	CD20 RECEPTOR	
41688	>10	R82942	Hs.107755	ESTs Weakly similar to GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE [E.coli]	

FIGURE 7 (CONT.)

32343	>10	R00965	Hs.125052	ESTs	
38335	>10	AA490916	Hs.112157	ESTs	
41729	>10	R02458	Hs.89554	Hemoglobin gamma-G	
36707	>10	AA434246	Hs.98802	EST	
28491	>10	C14784	Hs.12382	ESTs	
41702	>10	R06970	Hs.123363	ESTs	
32246	>10	R52163	Hs.144526	ESTs	
17314	>10	AA095487	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]	
30325	>10	N38967	Hs.44504	EST	
19823	>10	H58692	Hs.9520	ESTs Highly similar to FORMYL-TETRAHYDROFOLATE DEHYDROGENASE [Rattus norvegicus]	
42153	>10	T77729	Hs.89890	Pyruvate carboxylase	
19321	>10	H17511	Hs.24963	ESTs	
27110	>10	AA040494	Hs.84112	GTP synthetase	
28931	>10	D59722	Hs.92924	ESTs	
6333	>10	X82404	Hs.2653	Fibulin 2	
37679	>10	AA460661	Hs.99562	ESTs	
40828	>10	N84344	Hs.78362	Human clone 23839 mRNA sequence	
19132	>10	H09343	Hs.27261	ESTs	
19353	>10	H18706	Hs.31604	ESTs	
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]	
11621	>10	AA243574	Hs.14691	ESTs	
36538	>10	AA521370	Hs.104423	ESTs	
10095	>10	R22139	Hs.30343	ESTs	
30014	>10	N26740	Hs.42771	ESTs	
4464	>10	U44429	Hs.18611	Human D53 (hD53) mRNA partial cds	
3650	>10	U03877	Hs.78224	Human extracellular protein (S1-5) mRNA complete cds	
36377	>10	AA420058	Hs.99450	ESTs	
20437	>10	N50550	Hs.24587	Homo sapiens mRNA for E1a1 complete cds	
1576	>10	K02100	Hs.117050	ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR	
42078	>10	T64891	Hs.144323	ESTs	
27257	>10	AA418001	Hs.45146	ESTs Weakly similar to mitogen-activated kinase kinase 5 [H.sapiens]	
30582	>10	N49848	Hs.46974	EST	
3631	>10	U03090	Hs.290	Homo sapiens Ca2+-dependent phospholipase A2 mRNA complete cds	
19028	>10	H04768	Hs.30484	ESTs	
4752	>10	U59632	Hs.3947	Glycoprotein Ib (platelet) beta polypeptide	
3768	>10	U09579	Hs.74884	CYCLIN-DEPENDENT KINASE INHIBITOR 1	
1437	>10	J02923	Hs.76506	Lymphocyte cytosolic protein 1 (L-plasin)	
33905	>10	AFFX-		AFFX-TrpX-5	
4310	>10	U37055	Hs.76034	Macrophage stimulating 1 (hepatocyte growth factor-like)	
26923	>10	AA342302	Hs.55036	ESTs	

FIGURE 7 (CONT.)

5520	>10	X06258	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
37571	>10	AA457409	Hs.93458	EST
38800	>10	AA090952	Hs.112636	EST
27952	>10	AA463700	Hs.47042	Homo sapiens CD39L3 (CD39L3) mRNA complete cds
27621	>10	AA448242	Hs.55589	ESTs
38784	>10	AA609968	Hs.20351	Testis specific protein Y-linked
281	>10	D16532	Hs.73729	Very low density lipoprotein receptor
18014	>10	AA173168	Hs.57672	ESTs Weakly similar to myosin heavy chain [C.elegans]
16720	>10	AA044732	Hs.77208	ESTs
25336	>10	AA053405	Hs.101404	ESTs
2547	>10	M25809	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 58/58kD isoform 1
39953	>10	H56010	Hs.108144	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]
13777	>10	AA483504	Hs.6052	ESTs
13419	>10	AA450336	Hs.22268	ESTs
1403	>10	J00123	Hs.93557	PROENKEPHALIN A PRECURSOR
42373	>10	W35382	Hs.103012	ESTs
21520	>10	R28267	Hs.24258	ESTs
9706	>10	M63509	Hs.73974	Glutathione S-transferase M2 (muscle)
35950	>10	AA404271	Hs.22631	Human glutamate receptor (GLUR5) mRNA complete cds
42501	>10	W69586	Hs.103156	ESTs
33812	>10	Z41239	Hs.106960	ESTs
42473	>10	W63731	Hs.122531	ESTs
25195	>10	AA033790	Hs.75736	Apolipoprotein D
28607	>10	C21481	Hs.84630	ESTs Moderately similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]
3712	>10	U07620	Hs.89661	Human MAP kinase mRNA complete cds
6214	>10	X77307	Hs.2507	5-HYDROXYTRYPTAMINE 2B RECEPTOR
23575	>10	T80833	Hs.14794	ESTs
31775	>10	N79765	Hs.50847	ESTs
5206	>10	U82979	Hs.67846	Human clone HM18 monocyte inhibitory receptor precursor mRNA complete cds
22769	>10	R94521	Hs.124693	ESTs
9377	>10	H12674	Hs.5399	EST
29288	>10	H81046	Hs.70405	EST Moderately similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]
11061	>10	AA147537	Hs.4811	ESTs
41960	>10	T33511	Hs.4844	ESTs
20416	>10	H77734	Hs.35702	Homo sapiens roundsbout 1 (rbo1) mRNA complete cds
38248	>10	AA489218	Hs.105229	ESTs
37256	>10	AA449424	Hs.98428	ESTs
21911	>10	R43960	Hs.26320	ESTs
23184	>10	T34822	Hs.8108	ESTs Weakly similar to HYPOTHETICAL_35.8 KD PROTEIN IN PRP16-SRP40 INTERGENIC REGION [S.cerevisiae]
18225	>10	AA011305	Hs.10029	Calhepsin C

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FIGURE 7 (CONT.)

27766	>10	AA453656	Hs.89417	ESTs	
16071	>10	AA001426	Hs.40863	ESTs	
17343	>10	AA100152	Hs.5921	ESTs	
10643	>10	AA040154	Hs.32478	ESTs	
26335	>10	F68239	Hs.33122	ESTs	
34968	>10	AA344868	Hs.1265	Complement component 8 gamma polypeptide	
26303	>10	AA255483	Hs.88042	EST	
1030	>10	HG2416-		EST - HG2416-HT2512	
26370	>10	AA609559	Hs.38550	ESTs Moderately similar to alpha subunit [H.sapiens]	
29303	>10	H85881	Hs.38427	ESTs	
21078	>10	N99976	Hs.8018	ESTs	
27100	>10	AA040231		EST - RC_AA040231	
11329	>10	AA216589	Hs.28462	ESTs	
4402	>10	UA1518	Hs.74602	AQUAPORIN-CHIP	
11050	>10	AA142919	Hs.5558	ESTs	
22844	>10	R98947		EST - RC_R98947	
31581	>10	N71371	Hs.35938	ESTs	
7253	>10	AA074407	Hs.139119	ESTs	
20423	>10	N49308	Hs.104938	ESTs	
39264	>10	AA621750		EST - RC_AA621750	
36415	>10	AA426598	Hs.24897	Homo sapiens chromosome 21q22.1 anonymous mRNA sequence	
18575	>10	AA031948	Hs.57548	ESTs	
37505	>10	AA455659	Hs.103233	ESTs	
26264	>10	AA521080	Hs.46765	ESTs	
23886	>10	T95325	Hs.16545	ESTs	
11781	>10	AA256485	Hs.33413	ESTs	
25603	>10	AA114250	Hs.48924	Homo sapiens mRNA for KIAA0512 protein complete cds	
9003	>10	C00808	Hs.107882	ESTs	
5632	>10	X15357		EST - X15357	
7680	>10	AA206946	Hs.8059	ESTs	
22783	>10	R95689	Hs.35437	ESTs	
20852	>10	N69540	Hs.17713	ESTs	
16795	>10	AA047896	Hs.49169	ESTs	
37558	>10	AA456975	Hs.75736	Apolipoprotein D	
35957	>10	AA412537	Hs.98149	EST	
42129	>10	T71561	Hs.84824	ESTs	
34585	>10	AA2B1002	Hs.40735	ESTs	
33690	>10	Z38607	Hs.62248	ESTs	
8904	>10	AF002256	Hs.86180	Homo sapiens killer cell receptor (KIR103) mRNA allele ASD1 complete cds	
2689	>10	M32373	Hs.1256	Arylsulfatase B	

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FIGURE 7 (CONT.)

40909	>10	N69084	Hs.49608	ESTs	
22377	>10	R63090	Hs.28391	ESTs	
21208	>10	R07851	Hs.20023	EST	
27304	>10	AA421783	Hs.56808	Homo sapiens mRNA for zinc finger protein FPM315 complete cds	
3307	>10	M95809	Hs.89578	BASIC TRANSCRIPTION FACTOR 82 KD SUBUNIT	
25370	>10	AA057556	Hs.28478	ESTs	
41423	>10	R44717	Hs.22917	ESTs	
2570	>10	M27160	Hs.2053	Tyrosinase (oculocutaneous albinism IA)	
14557	>10	AA620965	Hs.108300	ESTs Highly similar to ADENYLOSUCCINATE SYNTHETASE MUSCLE ISOZYME [Mus musculus]	
7023	>10	Z78291	Hs.48607	EST - Z78291	
31051	>10	N62696	Hs.112956	EST	
39200	>10	AA621246	Hs.27457	ESTs	
24712	>10	Z39652	Hs.9444	ESTs Moderately similar to IIII ALU CLASS A WARNING ENTRY IIII [H.sapiens]	
23296	>10	T52497	Hs.134846	ESTs	
12826	>10	AA424808	Hs.75678	Human GOS3 mRNA complete cds	
2198	>10	L49169	Hs.43498	ESTs	
27228	>10	AA416767	Hs.8175	ESTs	
7135	>10	AA028976	Hs.8175	EST - RC_AA074955	
17102	>10	AA074955	Hs.94870	Human mRNA for KIAA0306 gene partial cds	
38942	>10	AA609646	Hs.38336	ESTs	
29288	>10	H64973	Hs.54434	Interferon regulatory factor 5	
34336	>10	AA250843	Hs.47681	ESTs	
30816	>10	N53568	Hs.65093	ESTs	
16739	>10	AA045461	Hs.113025	ESTs	
42317	>10	T97599	Hs.113025	EST - L77563	
2228	>10	L77563	Hs.47927	ESTs	
30862	>10	N55171	Hs.97951	ESTs	
35954	>10	AA412526	Hs.98467	ESTs	
36403	>10	AA426383	Hs.98467	ESTs	
36949	>10	AA441812	Hs.99559	ESTs	
41623	>10	R70212	Hs.79630	Immunoglobulin-associated alpha	
39175	>10	AA621078	Hs.111966	ESTs	
37657	>10	AA460147	Hs.98397	ESTs Weakly similar to precursor of major fibrous sheath protein [M.musculus]	
36279	>10	AA424242	Hs.2060	S100 calcium-binding protein A5 (formerly S100D)	
6634	>10	Z18954	Hs.107197	ESTs	
40562	>10	N33212	Hs.22636	ESTs	
13770	>10	AA463272	Hs.78362	Human clone 23839 mRNA sequence	
5101	>10	U79249	Hs.78362	Human transducin-like enhancer protein (TLE3) mRNA complete cds	
3355	>10	M99438	Hs.31305	Human transducin-like enhancer protein (TLE3) mRNA complete cds	
8476	>10	AA442119	Hs.29790	ESTs	

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FIGURE 7 (CONT.)

34231	>10	AA234527	Hs.75772	Glucocorticoid receptor
42046	>10	T59148	Hs.50966	Carbamoyl-phosphate synthetase 1 mitochondrial
23913	>10	T96123	Hs.17749	ESTs
37333	>10	AA452150	Hs.75122	TRANSFORMING PROTEIN RHOB
27946	>10	AA63434	Hs.42858	ESTs
34407	>10	AA255523	Hs.42858	EST - RC_AA255523
16542	>10	AA029428	Hs.61555	ESTs
6248	>10	X78712	Hs.98008	Glycerol kinase 2 (testis specific)
8227	>10	AA393686	Hs.75709	Mannose-6-phosphate receptor (calion dependent)
3507	>10	S78774	Hs.25717	EST - S78774
40907	>10	N86830	Hs.25717	ESTs
33340	>10	W78698	Hs.58550	ESTs
19079	>10	H06371	Hs.20945	ESTs
3992	>10	U19713	Hs.76364	Atograft inflammatory factor 1
36059	>10	AA417063	Hs.99189	ESTs
37634	>10	AA459582	Hs.99489	EST
41881	>10	R62313	Hs.126270	ESTs Weakly similar to RIT60 [R.norvegicus]
38734	>10	AA608792	Hs.112591	EST
37636	>10	AA470135	Hs.112238	ESTs
21303	>10	R11157	Hs.12610	ESTs
20125	>10	N22006	Hs.6202	ESTs
35516	>10	AA400795	Hs.97450	ESTs
26771	>10	AA284067	Hs.89287	EST
33558	>10	W90735	Hs.59332	EST
2830	>10	M57399	Hs.44	Pleiotrophin (heparin binding growth factor 8 neurite growth-promoting factor 1)
42625	>10	W89426	Hs.110128	ESTs
28152	>10	AA250845	Hs.87762	ESTs
31988	>10	N94581	Hs.55062	ESTs
17783	>10	AA148213	Hs.71873	ESTs Highly similar to 65 KO YES-ASSOCIATED PROTEIN (Gallus gallus)
21959	>10	R44949	Hs.22906	ESTs
10090	>10	N79674	Hs.7915	ESTs
30658	>10	N51105	Hs.111223	ESTs
17629	>10	AA131819	Hs.89009	ESTs
36260	>10	AA423970	Hs.98378	ESTs
285	>10	D16227	Hs.3818	Hippocalcin-like 1
26123	>10	AA243508	Hs.20887	ESTs
34535	>10	AA278391	Hs.104425	EST
29100	>10	H01428	Hs.92350	ESTs
24122	>10	W46947	Hs.4188	ESTs
19894	>10	H65942	Hs.36030	ESTs

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FIGURE 7 (CONT.)

22987	>10	T16258	Hs.25420	ESTs	
5985	>10	X64728	Hs.34514	H.sapiens CHML mRNA	
42461	>10	W62008	Hs.89717	Human preprocarboxypeptidase A2 (proCPA2) mRNA complete cds	
5422	>10	X00588	Hs.77432	Epidermal growth factor receptor	
16603	>10	AA034366	Hs.144627	ESTs	
33389	>10	W81607	Hs.58663	EST	
6931	>10	Z46788	Hs.3232	H.sapiens mRNA for cyclin II	
19324	>10	H17618	Hs.28180	ESTs	
32166	>10	R41836	Hs.9057	ESTs	
39987	>10	H58415	Hs.102160	EST	
17958	>10	AA168917	Hs.72639	ESTs	
39569	>10	AA598437	Hs.29385	ESTs Highly similar to MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 [Saccharomyces cerevisiae]	
1006	>10	HG2280-	EST - HG2260-HT2349		
23552	>10	T79638	Hs.105818	ESTs	
38228	>10	AA488997	Hs.137530	ESTs	
1066	>10	HG22705-	EST - HG2705-HT2801		
23815	>10	T91283	EST - RC_T91283	Human APEC-1 mRNA complete cds	
4699	>10	U57099	Hs.21639	ESTs	
31306	>10	N86796	Hs.144212	ESTs	
12389	>10	AA399633	Hs.24872	ESTs	
34539	>10	AA279662	Hs.142452	ESTs Moderately similar to snRNP protein B [H.sapiens]	
20358	>10	N35584	Hs.17404	ESTs	
26070	>10	AA238868	Hs.87564	ESTs	
38210	>10	AA488659	Hs.105686	ESTs	
26025	>10	AA235574	PUTATIVE DNA BINDING PROTEIN A20		
4978	>10	U71207	Hs.29279	Human sapiens clone 24534 eyes absent homolog (Eab1) mRNA partial cds	
3501	>10	U68162	Hs.84171	THROMBOPOIETIN RECEPTOR PRECURSOR	
14281	>10	S78467	EST - S78467	ESTs	
31859	>10	AA505136	Hs.12420	ESTs	
41104	>10	N90688	Hs.54643	EST	
5293	>10	R01398	EST - RC_R01398	Human DNA binding protein FKHL15 (FKHL15) mRNA complete cds	
3543	>10	S81957	EST - S81957	ESTs	
27615	>10	AA443958	Hs.90960	ESTs	
7152	>10	AA038753	Hs.78484	Home sapiens mRNA for KIAA0525 protein partial cds	
16197	>10	AA010328	Hs.39379	ESTs	
20178	>10	N24772	Hs.30213	Home sapiens putative transmembrane protein (CLN5) mRNA complete cds	
33586	>10	W83015	Hs.73166	Treacher Collins syndrome susceptibility protein	
27265	>10	AA418392	Hs.46784	ESTs	
12453	>10	AA402000	Hs.20415	ESTs Weakly similar to GS3786 [H.sapiens]	

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FIGURE 7 (CONT.)

36302	>10	AA424652	Hs.124955	ESTs	
23192	>10	T40448	Hs.8204	ESTs	
17423	>10	AA114071	Hs.26270	ESTs	
23464	>10	T67026	Hs.13019	ESTs	
42762	>10	Z41697	Hs.106296	ESTs	
32628	>10	T56470	Hs.119190	Chromogranin A (parathyroid secretory protein 1)	
12805	>10	AA424331	Hs.28640	ESTs	
25379	>10	AA058803	Hs.111841	Human adenyl cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds	
39318	>10	C20817	Hs.108945	Homo sapiens mRNA for KIAA0515 protein partial cds	
29699	>10	H97938	Hs.75772	Glucocorticoid receptor	
17507	>10	AA160530	Hs.72447	ESTs	
35810	>10	AA411011	Hs.8038	ESTs	
36838	>10	AA436163	Hs.95851	Homo sapiens Fig12 (FIG12) mRNA complete cds	
29611	>10	H94043	Hs.41949	ESTs	
10650	>10	H46167	Hs.31542	ESTs	
33221	>10	W70305	Hs.64659	ESTs	
18940	>10	F10265	Hs.13287	ESTs	
2580	>10	M27533		EST - M27533	
7274	>10	AA082171	Hs.8261	ESTs	
19524	>10	H29568	Hs.83466	Homo sapiens clone 23579 mRNA sequence	
40571	>10	N33558	Hs.103102	ESTs Weakly similar to WWP2 [H.sapiens]	
31178	>10	N64191	Hs.46584	ESTs	
29694	>10	N23009	Hs.43296	ESTs	
22201	>10	RS4416	Hs.140932	ESTs	
28719	>10	AA282583	Hs.88517	ESTs	
32493	>10	T16497	Hs.85339	EST	
37179	>10	AA448004	Hs.69150	ESTs	
17990	>10	AA169173	Hs.72754	ESTs	
21934	>10	R44449	Hs.48778	ESTs	
36792	>10	AA435848		EST - RC_AA435848	
34056	>10	AA194851	Hs.110575	ESTs	
39102	>10	AA620674	Hs.112882	EST	
26283	>10	AA253217	Hs.41271	ESTs	
23889	>10	T98529	Hs.16398	ESTs	
32456	>10	T15929	Hs.65284	ESTs	
15440	>10	W27301	Hs.111652	ESTs Moderately similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA [Thermomonas curvata]	
19004	>10	H03299	Hs.30390	EST	
27839	>10	AA456309	Hs.58831	ESTs	
18848	>10	F10338	Hs.106309	ESTs Moderately similar to FOG [M.musculus]	
13112	>10	AA435896	Hs.16397	ESTs	

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FIGURE 7 (CONT.)

1850	>10	L17325	Hs.278	Human pre-TANK cell associated protein (1D12A2) mRNA complete cds
9101	>10	C17938	Hs.25536	ESTs
2807	>10	M55210	Hs.87428	Laminin gamma 1 (formerly LAMB2)
3383	>10	S37153	Hs.91787	Retinoblastoma-binding protein 1 (alternative products)
23142	>10	T26444	Hs.101248	ESTs
5367	>10	U95018	Hs.30941	Myasthenic syndrome antigen B (human fetal brain mRNA 3477 nt)
32205	>10	R44234	Hs.75169	ESTs
28515	>10	AA262972	Hs.87298	ESTs
15332	>10	W24127	Hs.16003	ESTs Weakly similar to keratin 8 type II cytoskeletal embryonic (M.musculus)
34183	>10	AA232251	Hs.128530	ESTs
6392	>10	X85753	Hs.25283	CELL DIVISION PROTEIN KINASE 8
33784	>10	Z40689	Hs.65973	ESTs
33474	>10	W87484	Hs.50429	ESTs
34984	>10	AA344854	Hs.96837	ESTs
14584	>10	AA821414	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
22640	>10	R83684	Hs.33416	EST
4339	>10	U38372	EST - U38372	
37567	>10	AA456988	Hs.41548	Human MHC Class I region proline rich protein mRNA complete cds
4937	>10	U68385	Hs.117313	Human Meis1-related protein 2 (MRG2) mRNA partial cds
30795	>10	N53043	Hs.47606	ESTs
30966	>10	N59432	Hs.48382	EST
33991	>10	AA181935	Hs.104050	EST
2285	>10	M11591	EST - M11591	
24315	>10	W84413	Hs.23017	ESTs
38752	>10	AA608852	Hs.112603	EST
5116	>10	U78271	Hs.7571	Human clones 23920 and 23921 mRNA sequence
15037	>10	U44798	Hs.93502	Human U1-sRNP binding protein homolog mRNA complete cds
37045	>10	AA446000	Hs.99043	ESTs
37627	>10	AA459392	Hs.105042	ESTs
21935	>10	R44477	Hs.22848	ESTs
18669	>10	F03869	Hs.27278	ESTs Highly similar to PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [Bos taurus Sus scrofa]
22737	>10	R92512	EST - RC_R92512_s	
30727	>10	N51987	Hs.47390	EST
16086	>10	AA001879	Hs.59890	EST
23293	>10	T52201	Hs.9410	ESTs
5294	>10	U90065	Hs.79351	Human Iwo P-domain K+ channel TWIK-1 mRNA complete cds
17769	>10	AA148923	Hs.93675	ESTs
25549	>10	AA101056	EST - RC_AA101056	
84	>10	AF001359	EST - AF001359_J	
4856	>10	U65093	Human msg1-related gene 1 (msg1) mRNA complete cds	

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FIGURE 7 (CONT.)

7697	>10	AA214730	Hs.107256	ESTs	
36295	>10	AA24535	Hs.98416	ESTs	
17490	>10	AA125781	Hs.57489	ESTs	
36976	>10	AA42779	Hs.98983	ESTs	
10425	>10	AA010819	Hs.16446	ESTs	
41196	>10	R11654	Hs.20526	ESTs	
42285	>10	T94409	EST - RC_T94409	EST	
33185	>10	W69435	Hs.58009	EST	
13974	>10	AA470299	Hs.21107	ESTs	
19868	>10	H81580	EST - RC_H81580	ESTs	
1378	>10	HG831-	EST - HG831-HT831	EST	
621	>10	D53813	Hs.26886	Human mRNA for rod photoreceptor protein complete cds	
5346	>10	U92459	Hs.86204	Human melastrophin glutamate receptor 8 mRNA complete cds	
6029	>10	X69533	Hs.77890	GUANYLATE CYCLASE SOLUBLE BETA-1 CHAIN	
22196	>10	R53972	Hs.26026	ESTs	
24609	>10	Z38900	Hs.26815	ESTs	
37198	>10	AA448228	EST - RC_AA448228	ESTs	
26151	>10	AA250838	Hs.108509	ESTs	
5938	>10	X62535	Hs.74044	Diacylglycerol kinase alpha (80kD)	
16373	>10	AA019603	Hs.60992	ESTs	
28356	>10	AA609080	Hs.41585	ESTs	
20070	>10	H88854	Hs.20423	ESTs	
17717	>10	AA136541	Hs.71647	EST	
20059	>10	H98768	Hs.13121	ESTs	
40865	>10	N74604	Hs.124694	ESTs	
10194	>10	R63545	Hs.11553	ESTs Weakly similar to putative type III alcohol dehydrogenase (D.melanogaster)	
40200	>10	H87229	Hs.82963	Gonadotropin-releasing hormone (leulinizing-releasing hormone)	
34863	>10	AA347417	Hs.96869	EST	
23543	>10	T79203	Hs.14480	ESTs	
12770	>10	AA421778	Hs.8981	ESTs	
25085	>10	AA017518	Hs.115241	Homo sapiens G protein beta 5 subunit mRNA complete cds	
37746	>10	AA463627	Hs.95598	ESTs	
2370	>10	M16505	Hs.79076	STERYL-SULFATASE PRECURSOR	
31244	>10	N66062	Hs.49112	EST	
31716	>10	N75507	Hs.50628	ESTs Weakly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP17 [Rattus norvegicus]	
28308	>10	AA598959	Hs.59183	ESTs	
2220	>10	L76687	Hs.83070	Homo sapiens Gb14 mRNA complete cds	
12404	>10	AA400292	Hs.23786	ESTs	
41050	>10	N92882	Hs.109494	ESTs Weakly similar to putative progesterone binding protein [H.sapiens]	
2407	>10	M18737	Hs.90708	GRANZYME A PRECURSOR	

FIGURE 7 (CONT.)

23462	>10	T69948	Hs.12992	ESTs	
16614	>10	F02418	Hs.107614	ESTs	
40553	>10	N32060	Hs.104010	Homo sapiens CAG-isl 7 mRNA complete cds	
27828	>10	AA455949	Hs.61232	ESTs	
207	>10	D12763	Hs.66	Suppression of tumorigenicity 2	
41064	>10	N63508	Hs.102923	EST	
10845	>10	AA084405	Hs.106313	ESTs Weakly similar to P24 protein [M.musculus]	
21813	10	R42039	Hs.23084	ESTs	
19463	10	AA233151	Hs.81796	ESTs	
17507	10	AA125419	Hs.74876	ESTs	
23957	10	T97487	Hs.18070	ESTs	
13317	10	AA448212	Hs.38095	ESTs	
29550	10	H90133	Hs.41352	ESTs	
39068	10	AA620411	Hs.141503	Small inducible cytokine A5 (RANTES)	
28620	10	AA280413	Hs.89843	Spleen focus forming virus (SFFV) proviral integration oncogene spl1	
37675	10	AA460377	Hs.99816	ESTs	
31437	10	N68921	Hs.49573	ESTs	
32657	10	T68867	Hs.76889	ESTs	
34952	10	AA342028	Hs.73734	PLATELET GLYCOPROTEIN V PRECURSOR	
26475	10	AA262264	Hs.87640	ESTs	
41827	10	T15445	Hs.99491	H.sapiens mRNA for F2593.3 kinase like protein from C.elegans	
20073	10	H98985	Hs.111911	ESTs	
42336	10	T99713	Hs.139933	ESTs	
26412	10	AA258224	Hs.86646	ESTs	
21352	10	R15890	Hs.21745	ESTs	
22583	10	R79239	Hs.29855	EST	
34020	10	AA191543	Hs.144302	EST	
25913	10	AA161105	EST - RC_AA161105	Homo sapiens transmembrane protein mRNA complete cds	
82	10	AF000959	Hs.110903	ESTs	
37531	10	AA456140	Hs.99235	ESTs	
13314	10	AA448169	Hs.6728	EST - RC_N66510	
31430	10	N68610	Hs.46633	EST	
30570	10	N49587	Hs.103568	EST	
7302	10	AA089688	Hs.103568	EST	
27732	10	AA452167	Hs.55778	ESTs	
22533	10	R73408	Hs.140996	ESTs	
31079	10	N62969	Hs.48932	EST	
35470	10	AA400393	Hs.97803	EST Weakly similar to precursor polypeptide [H.sapiens]	
37102	10	AA446889	Hs.119316	ESTs	
203	10	D12620	Hs.105242	CYTOCHROME P450 IVF3	

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FIGURE 7 (CONT.)

11427	10	AA233277	Hs.74947	ESTs	
24159	10	W57862	Hs.21289	ESTs	
17870	10	AA151772	Hs.72185	ESTs	
5302	10	U90543	Hs.79041	Human butyrophilin (BTF1) mRNA complete cds	
27256	10	AA417998	Hs.62781	ESTs	
2219	10	L76670	Hs.109610	Homo sapiens nkal7 mRNA complete cds	
30658	10	N55081	Hs.47915	EST	
8870	10	AB002387	Hs.21355	Human mRNA for KIAA0369 gene complete cds	
40870	10	N67262	Hs.358	Zinc finger protein 135 (clone pHZ-17)	
11811	10	AA258130	Hs.11530	ESTs	
33254	10	W72833	Hs.58187	ESTs	
17192	10	AA078094	EST - RC_AA078094		
24392	10	W88568	Hs.58589	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds	
27456	10	AA430539	Hs.57760	ESTs	
25419	10	AA069386	EST - RC_AA069386		
7100	10	AA012985	Hs.50548	ESTs	
31588	10	N71571	Hs.50050	ESTs	
29995	10	N26401	Hs.43802	EST	
31973	10	N93875	Hs.55015	EST	
36159	10	AA418279	Hs.82813	Colony-stimulating factor 1 (M-CSF)	
12419	10	AA400888	Hs.7159	ESTs	
27076	10	AA401630	Hs.62592	ESTs	
28251	10	AA904512	Hs.76852	ESTs Weakly similar to ZK782.1 [C.elegans]	
4219	10	U32324	Hs.64310	Human Interleukin-11 receptor alpha chain mRNA complete cds	
27991	10	AA465650	Hs.87306	ESTs	
37702	10	AA461119	Hs.99539	ESTs	
25251	10	AA040792	Hs.54421	Bradykinin receptor B2	
27064	10	AA401253	Hs.87677	ESTs	
37582	10	AA458668	Hs.95698	ESTs	
39619	9	F10840	Hs.12354	ESTs	
31053	9	N62724	Hs.48614	EST	
33338	9	W79524	Hs.58585	ESTs	
23368	9	T59005	Hs.10476	EST	
6240	9	AA397841	Hs.108879	ESTs	
21778	9	R41389	Hs.29159	EST	
31168	9	N63965	Hs.48903	ESTs	
3440	9	S72370	Hs.89890	Pyruvate carboxylase	
25930	9	AA164928	EST - RC_AA164928		
29571	9	N25657	Hs.83892	EST	
39771	9	H117463	Hs.101735	ESTs	

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FIGURE 7 (CONT.)

21481	9	R26141	Hs.24032	ESTs Highly similar to transmembrane receptor [M.musculus]
10887	9	AA101832	Hs.22971	ESTs
31431	9	N68666	Hs.76798	ESTs
30756	9	N52398	Hs.39252	ESTs
35829	9	AA411438	Hs.74635	Dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex 2-oxo-glutarate complex branched chain keto acid dehydrog
24540	9	Z38435	Hs.19235	ESTs
37500	9	AA455474	Hs.100530	ESTs
19007	9	H03358	EST - RC_H03358	EST
42650	9	W92272	Hs.25601	Homo sapiens zinc-finger helix (hZFh) mRNA complete cds
16705	9	AA043675	Hs.62633	EST
40275	9	H94547	Hs.102329	ESTs
24372	9	W87423	Hs.35598	ESTs
9011	9	C01394	Hs.106823	Homo sapiens clone 24818 mRNA sequence
40780	9	N59568	Hs.108107	ESTs
17177	9	AA079331	EST - RC_AA079331	EST
20878	9	N70305	Hs.34492	ESTs
38140	9	AA486273	Hs.100472	ESTs
3490	9	S77763	Hs.75643	Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds
39112	9	AA620724	Hs.112890	ESTs
27347	9	AA424940	Hs.43580	ESTs
14747	9	D60364	Hs.34882	ESTs
23590	9	T82307	EST - RC_T82307	EST
23979	9	T98262	EST - RC_T98262	EST
27759	9	AA453472	Hs.95111	ESTs
36691	9	AA432381	Hs.97357	ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE [H.sapiens]
26782	9	AA284181	Hs.89310	ESTs
26818	9	AA285145	Hs.50446	ESTs
22334	9	R61290	Hs.25870	ESTs
22945	9	N22995	Hs.42829	ESTs
22945	9	T10134	Hs.9877	Homo sapiens mRNA for KIAA0688 protein complete cds
30518	9	N50656	It.93596	ESTs Highly similar to mosaic protein LR11 [H.sapiens]
29715	9	H98700	Hs.60897	ESTs
37560	9	AA457023	EST - RC_AA457023	EST
23264	9	T50052	Hs.9092	EST
31001	9	N62200	Hs.47566	ESTs
17841	9	AA156109	Hs.66180	ESTs
3478	9	S76992	Hs.104005	Vav 2 oncogene
11605	9	AA243139	Hs.4863	ESTs
19032	9	H04822	Hs.30494	EST
29933	9	N24182	Hs.93677	ESTs

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FIGURE 7 (CONT.)

26522	9	AA280431	Hs.88756	ESTs	Human repressor transcriptional factor (ZNF85) mRNA complete cds
4289	9	U35376	Hs.37138	ESTs	Human metallothionein (MT)-I gene
42034	9	T56281	Hs.110440	ESTs	EST - RC_AA039568
30447	9	N47439	Hs.44603	ESTs	EST - RC_AA039568
25238	9	AA039568	Hs.14855	ESTs	EST - RC_AA039568
20238	9	N30077	Hs.44600	EST	EST - RC_AA039568
30232	9	N34500	Hs.10839	EST	EST - RC_AA039568
17017	9	AA059920	Hs.10839	EST	EST - RC_AA039568
11845	9	AA259064	Hs.10839	EST	EST - RC_AA039568
30229	9	N34457	Hs.47442	EST	EST - RC_AA039568
30737	9	N52137	Hs.47442	EST	EST - RC_AA039568
30555	9	N49259	Hs.47442	EST	EST - RC_AA039568
981	9	HG2139-	Hs.93956	EST	EST - RC_AA039568
30498	9	N48325	Hs.93956	EST	EST - RC_AA039568
40434	9	N21461	Hs.95594	EST	EST - RC_AA039568
36788	9	AA435824	Hs.95594	EST	EST - RC_AA039568
28991	9	F04852	Hs.66195	ESTs	EST - RC_AA039568
25942	9	AA234187	Hs.87267	ESTs	EST - RC_AA039568
30466	9	N47951	Hs.57485	ESTs	EST - RC_AA039568
19317	9	H17476	Hs.11615	ESTs	EST - RC_AA039568
13859	9	AA470068	Hs.24309	ESTs	EST - RC_AA039568
23445	9	T65992	Hs.11722	EST	EST - RC_AA039568
24448	9	V93273	Hs.9270	ESTs	EST - RC_AA039568
7583	9	AA167824	Hs.63559	ESTs	EST - RC_AA039568
22778	9	R84840	Hs.35372	ESTs	EST - RC_AA039568
16439	9	AA024835	Hs.47584	ESTs	EST - RC_AA039568
42395	9	W42733	Hs.109870	ESTs	EST - RC_AA039568
19991	9	HQ0887	Hs.18357	ESTs	EST - RC_AA039568
23690	9	T87648	Hs.125175	ESTs	EST - RC_AA039568
7111	9	AA018804	Hs.54421	ESTs	EST - RC_AA039568
6400	9	X86163	Hs.54421	ESTs	EST - RC_AA039568
42474	9	W63747	Hs.109818	ESTs	EST - RC_AA039568
11425	9	AA233257	Hs.25511	ESTs	EST - RC_AA039568
27039	9	AA400277	Hs.48849	ESTs	EST - RC_AA039568
32206	9	R44386	Hs.91703	ESTs	EST - RC_AA039568
13310	9	V19098	Hs.7921	ESTs	EST - RC_AA039568
36501	9	AA431337	Hs.98017	ESTs	EST - RC_AA039568
463	9	D38462	Hs.50482	ESTs	EST - RC_AA039568
31674	9	N74357	Hs.50482	ESTs	EST - RC_AA039568
31182	9	N64339	Hs.48956	EST	EST - RC_AA039568

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FIGURE 7 (CONT.)

13499	AA453458	Hs.7301	ESTs	
37514	AA455914	Hs.1019	Parathyroid hormone receptor, 1	
5998	X55644	Hs.75063	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2	
962	HG180-		EST - HG180-HT180	
40790	N62328	Hs.3788	Glutamate receptor metabotropic 3	
25700	AA131512	Hs.103820	EST	
36880	AA435708	Hs.98895	ESTs	
2809	M55267	Hs.41848	EV12A PROTEIN PRECURSOR TROPIC VIRAL INTEGRATION SITE 2A PROTEIN)	
5620	X14885	Hs.2025	Transforming growth factor beta 3	
16643	AA033325	Hs.47200	ESTs	
32051	R01450	Hs.91081	ESTs	
33550	V80617	Hs.50120	ESTs	
6177	X75535	Hs.110884	33 KD HOUSEKEEPING PROTEIN	
33000	W45531	Hs.94642	ESTs	
20668	H98701	Hs.4985	ESTs	
4590	U50534	Hs.30649	Human infant brain mRNA clone 13cDNAT3	
37199	AA448257	Hs.97127	ESTs	
24601	Z38844	Hs.25803	ESTs	
33589	W93074	Hs.59342	ESTs	
37389	AA453468	Hs.59330	ESTs	
5801	X55448	Hs.3118	H.sapiens mRNA for 2.19 gene	
28748	D25912	Hs.74832	ESTs	
40070	H72592	Hs.77554	ESTs	
40367	H98857	Hs.75520	Human mRNA for KIAA0041 gene partial cds	
33609	W93585	Hs.59476	ESTs	
24502	Z38214	Hs.26946	ESTs	
11129	AA156873	Hs.15970	ESTs	
7144	AA033659	Hs.95154	ESTs	
28584	C21221	Hs.68619	ESTs highly similar to METALLOTHIONEIN-1A [Equus caballus]	
22165	R52822	Hs.22003	ESTs	
31987	N94551	Hs.55060	ESTs	
32470	T15956	Hs.65289	EST	
36642	AA599152	Hs.91379	PTD-ASSOCIATED SPLICING FACTOR	
40438	N21864	Hs.80500	Human mRNA for KIAA0061 gene partial cds	
34471	AA258843	Hs.111376	ESTs	
41571	R61005	Hs.115170	Homo sapiens mRNA for GalT4 protein	
31417	N68435	Hs.49516	ESTs	
23951	T97318	Hs.18037	ESTs	
7832	AA249260	Hs.28545	ESTs	
27928	AA461083	Hs.26789	ESTs Moderately similar to zinc finger protein [R.norvegicus]	

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FIGURE 7 (CONT.)

2017	L34219	Hs.1933	Cellular retinoid-binding protein
25530	AA098834	Hs.83428	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
20556	N55189	Hs.34081	ESTs
27036	AA400155	Hs.142935	ESTs
22651	R85266	Hs.33487	ESTs
31663	W95805	Hs.59736	EST
18374	H19472	Hs.31653	EST
10275	R79356	Hs.19280	ESTs Weakly similar to PROTEIN Q300 [Mus musculus]
39471	D60265	Hs.107894	ESTs
25100	AA019426	Hs.103343	EST
8828	AB002316	Hs.55746	Human mRNA for KIAA0318 gene partial cds
17132	AA075674	Hs.82577	EST - RC_AA075674
15915	Y08858	Hs.6723	Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34)) hypothetical prote
8216	AA393089	Hs.29196	ESTs
22512	R71489	Hs.30842	EST
19097	H08171	Hs.130843	ESTs
25048	AA011041	Hs.97699	ESTs
35353	AA398962	Hs.49193	EST
31278	N68399	Hs.7569	EST
23149	T26893	Hs.22057	ESTs
11880	AA262783	Hs.71018	ESTs
17547	AA127595	Hs.55501	ESTs
32054	W32094	Hs.98852	EST
36822	AA435978	Hs.41717	Human 3' cyclic nucleotide phosphodiesterase (HSPDE 1A3A) mRNA complete cds
35530	AA400893	Hs.106185	Human Rad guanine nucleotide dissociation stimulator mRNA partial cds
3869	U14417	Hs.100739	ESTs
9386	H09246	Hs.111075	Human orphan G-protein coupled receptor Dez isoform a mRNA complete cds
15154	U79527	Hs.19748	EST
21178	R08607	Hs.56213	ESTs
33081	W57731	Hs.21323	ESTs
13848	AA465664	Hs.13258	ESTs
18659	F03220	Hs.1964	Solute carrier family 5 (sodium/glucose cotransporter) member 1
1979	L29339	Hs.29378	ESTs
22609	R00945	Hs.1817	Myeloperoxidase
2418	M19507	Hs.124418	ESTs
28853	D80051	Hs.51501	ESTs
26764	AA283326	Hs.59096	EST - X95877
6544	X95877	Hs.87624	ESTs
33524	W89188	Hs.87624	ESTs
18374	AA226877	Hs.87624	ESTs

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FIGURE 7 (CONT.)

10108	7	R25069	Hs.23760	ESTs	Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP-1) mRNA complete cds
26178	7	AA251153	Hs.27910	ESTs	Human cardiac myosin binding protein-C (MyBP-C) gene complete cds
36428	7	AA427605	Hs.99551	EST	
29808	7	N21032	Hs.42931	ESTs	
24837	7	Z41186	Hs.27997	ESTs	
24909	7	Z98482	Hs.27250	ESTs	
26333	7	AA256075	Hs.92280	ESTs	Homo sapiens regulator of G protein signaling 10 mRNA complete cds
11507	7	AA235465	Hs.29161	ESTs	
40387	7	H99460	Hs.109873	ESTs	
16112	7	AA004377	Hs.91813	ESTs	Human butyrophilin (BTf2) mRNA complete cds
25413	7	AA065096	Hs.20887	ESTs	EST - RC_AA065096
13232	7	AA443944	Hs.67805	ESTs	
27236	7	AA417037	Hs.129672	ESTs	
21684	7	R38944	Hs.15301	ESTs	
9284	7	D82712	Hs.5091	ESTs	ESTs Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BarnHI-ori7 protein [C. elegans]
16886	7	AA057119	Hs.28029	ESTs	Homo sapiens torsinB (DO1) mRNA partial cds
20083	7	H99879	Hs.36572	ESTs	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus]
30851	7	N51029	Hs.22123	ESTs	
22362	7	R62447	Hs.23076	ESTs	
21581	7	R33245	Hs.23076	ESTs	
21636	7	R37501	Hs.110130	ESTs	Homo sapiens chromosome 19 cosmid F22329
21223	7	R08175	Hs.1339	ESTs	Collagen type IV alpha 2
32218	7	R45654	Hs.25722	ESTs	ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens]
13405	7	AA450118	Hs.47111	ESTs	
30827	7	N50740	Hs.44227	ESTs	ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H. sapiens]
30117	7	N30824	Hs.105669	ESTs	EST - RC_N67238
31344	7	N67238	Hs.105715	ESTs	
38119	7	AA485714	Hs.82401	ESTs	CD69 antigen (early T cell activation antigen)
33297	7	W73761	Hs.24550	ESTs	
6892	7	Z30426	Hs.13021	ESTs	
9923	7	N44998	Hs.95464	ESTs	ESTs Moderately similar to transcription enhancer factor TEF1 [H. sapiens]
27842	7	AA463237	Hs.43005	ESTs	
34845	7	AA283420	Hs.85280	ESTs	Human interferon regulatory factor 7 (humirf7) mRNA complete cds
29829	7	N21460	Hs.112083	ESTs	
15059	7	U53831	Hs.109558	ESTs	
40441	7	N22053	Hs.62542	ESTs	Acylxylase (neutrophil)
25095	7	AA018937	Hs.89949	ESTs	Epoxide hydrolase 1 (microsomal xenobiotic)
2941	7	M62840	Hs.79310	ESTs	Human GAP SH3 binding protein mRNA complete cds
1845	7	L25878			
42648	7	W92150			

FIGURE 7 (CONT.)

19592	7	H40696	Hs.33750	ESTs	
29801	7	N20939	Hs.38759	ESTs	
15417	7	W26982	Hs.39330	ESTs	
39877	7	H38627	Hs.107606	ESTs	
23967	7	T97910	Hs.18184	EST	
20041	7	H97012	Hs.11050	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]	
18314	7	AA214510	Hs.85518	ESTs	
22452	7	R67370	Hs.28758	ESTs	
30496	7	N48294	Hs.46950	EST	
26830	7	AA287057	Hs.48820	ESTs	
33432	7	W66075	Hs.38715	ESTs	
31394	7	N67990	Hs.49421	ESTs	
7053	6	Z84721	Hs.75792	Hemoglobin alpha 1	
33518	6	W68999	Hs.59134	EST	
5355	6	U94320	Hs.123021	Human Y5 receptor mRNA complete cds	
41311	6	R38516	Hs.124255	EST	
12545	6	AA406320	Hs.24702	ESTs	
23843	6	T82561	Hs.110422	ESTs	
21687	6	R38475	Hs.21408	ESTs	
17472	6	AA121704	Hs.69494	ESTs	
25648	6	AA126873	Hs.110341	ESTs	
32710	6	T87324	Hs.91021	EST	
3450	6	S73840	Hs.931	Hs spleen mRNA for fast 2a myosin heavy chain (3' end)	
979	6	HG20900-		EST - HG20900-HT12152	
8151	6	AA346686		EST - AA346686	
35380	6	AA399522	Hs.97571	ESTs Weakly similar to T04A8.9 [C.elegans]	
23789	6	T91047	Hs.128785	ESTs	
940	6	HG1496-		EST - HG1496-HT1496	
35896	6	AA412106	Hs.97349	ESTs	
15350	6	AA019034	Hs.94000	ESTs	
27547	6	AA436613	Hs.72157	ESTs	
22528	6	R73036	Hs.29323	EST	
25815	6	AA149889	Hs.96200	ESTs Weakly similar to A-kinase anchor protein 85 AKAP85 [R.norvegicus]	
8473	6	AA437346	Hs.2957	SHB adaptor protein (a Src homology 2 protein)	
35742	6	AA406058	Hs.97999	EST	
36538	6	AA430002	Hs.112044	ESTs	
17831	6	AA152323	Hs.71947	ESTs	
25072	6	AA015799	Hs.33792	ESTs	
15632	6	W66102	Hs.71218	ESTs	
20442	6	N50827	Hs.25275	ESTs	

FIGURE 7 (CONT.)

28357	6	AA609120	Hs.55185	ESTs Weakly similar to The KIAA0147 gene product is related to adenylyl cyclase, [H.sapiens]
25022	6	AA007591	Hs.110227	ESTs
29134	6	H68158	Hs.28310	ESTs
28148	6	AA488875	Hs.6433	Homo sapiens clone 24523 mRNA sequence
30744	6	N52185	Hs.105365	H.sapiens mRNA for arginine methyltransferase
27577	6	AA442090	Hs.119295	ESTs
33472	6	W87469	Hs.58992	ESTs
25687	6	AA130857	Hs.100119	ESTs
10549	6	AA027317	Hs.19138	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY [H.sapiens]
32835	6	W23631	Hs.55428	ESTs
17025	6	AA070160	EST - RC_AA070160	ESTs
22039	6	T10070	Hs.4217	Homo sapiens mRNA for KIAA0987 protein partial cds
15803	6	X52332	Hs.104115	Human Kox1 gene for Zinc finger protein
34618	6	AA282143	Hs.58094	H.sapiens mRNA for melanoma growth regulatory protein MIA
11074	6	AA148983	Hs.29068	ESTs
12212	6	AA287746	Hs.22554	ESTs
16102	6	AA002150	Hs.58872	ESTs
31340	6	N67197	Hs.50125	EST
19459	6	H24317	Hs.6528	ESTs
17533	6	AA127058	Hs.71057	EST
22017	6	R46597	Hs.22703	ESTs
23587	6	T87519	Hs.16075	ESTs Weakly similar to no similarities to reported gene products [H.sapiens]
30298	6	N38130	Hs.44792	EST Weakly similar to hypothetical protein [H.sapiens]
28973	6	F04014	Hs.65995	ESTs
17042	6	AA070387	EST - RC_AA070387	ESTs
20817	6	N68628	Hs.37630	ESTs
18430	6	AA232138	Hs.118898	ESTs
28493	6	C14820	Hs.67188	EST
30407	6	N48302	Hs.46852	EST
32502	6	T16886	Hs.65373	ESTs
41324	6	R38804	Hs.13434	Homo sapiens clone 24418 mRNA sequence
18418	6	AA228096	Hs.60480	ESTs
23622	6	T84046	Hs.15345	ESTs
15342	6	W25781	Hs.8136	Homo sapiens clone 23638 mRNA sequence
15248	6	W01094	Hs.84628	ESTs
2247	6	M10321	Hs.110802	VON WILLERAND FACTOR PRECURSOR
31906	6	N02643	Hs.35986	Homo sapiens CASK mRNA complete cds
9062	6	C06238	Hs.95685	Homo sapiens clone 24700 unknown mRNA partial cds
38640	6	AA599142	Hs.112509	EST
42622	6	W87801	Hs.106209	ESTs

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FIGURE 7 (CONT.)

27908	6	AA460571	Hs.54837	ESTs	
7293	6	AA085354	EST - AA085354	ESTs	
27322	6	AA424325	Hs.40495	ESTs	
5774	6	X54199	Hs.82205	Phosphoribosylglycinamide formyltransferase phosphoribosylglycinamide synthetase phosphoribosylaminimidazole synthetase	
33469	6	W87454	Hs.58987	ESTs Highly similar to homogenisate 12-dioxygenase (H.sapiens)	
40329	6	H87488	Hs.108802	Human N-ethylmaleimide-sensitive factor mRNA partial cds	
26339	6	AA278548	Hs.88522	ESTs	
23579	6	T81098	Hs.124065	ESTs	
22435	6	R66706	Hs.28708	ESTs	
19956	6	H80842	Hs.37445	ESTs	
18607	6	F02345	Hs.21197	ESTs	
18991	6	H02554	Hs.30323	ESTs	
7810	6	AA248169	Hs.105709	ESTs Highly similar to LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR [Rattus norvegicus]	
30810	6	N53419	Hs.47646	ESTs	
17996	6	AA169606	Hs.72815	ESTs	
26245	6	AA252357	Hs.87794	ESTs	
13348	6	AA449267	Hs.17914	ESTs Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT [M.musculus]	
15034	6	U43701	U43701	603 RIBOSOMAL PROTEIN L23A	
33802	6	Z41058	Hs.79248	ESTs	
33394	6	W84432	Hs.58670	ESTs	
31170	6	N54017	Hs.48911	ESTs	
40828	6	N64144	Hs.102749	EST	
17740	5	AA142922	Hs.936	Solute carrier family 17 (sodium phosphate) member 2	
9509	5	H58970	Hs.9817	Homo sapiens Arg/Abi-interacting protein ArgBP2a (ArgBP2a) mRNA complete cds	
15540	5	W30895	Hs.7535	ESTs	
27827	5	AA455976	Hs.42355	ESTs	
30697	5	N51585	Hs.47049	ESTs	
40299	5	H85787	Hs.108745	ESTs	
16627	5	AA036779	Hs.61826	Homo sapiens clone 23928 mRNA sequence	
20659	5	N62915	Hs.57672	ESTs Weakly similar to weakly similar to myosin heavy chain [C.elegans]	
31009	5	N62272	Hs.48502	ESTs	
14877	5	T65508	Hs.14623	Homo sapiens mRNA for KIAA0825 protein partial cds	
22830	5	N83178	Hs.48178	ESTs	
22830	5	R99421	EST - RC_R99421	ESTs	
25248	5	AA040507	Hs.92924	ESTs	
32145	5	R38910	Hs.66170	Homo sapiens clone 24503 mRNA sequence	
27970	5	AA454626	Hs.10247	Activated leucocyte cell adhesion molecule	
34508	5	AA262874	Hs.111394	ESTs	
29522	5	H88338	Hs.90250	ESTs	

FIGURE 7 (CONT.)

32159	5	R40974	Hs.124270	ESTs	
35492	5	AA400514	Hs.97505	ESTs	
37630	5	AA459649	Hs.95485	ESTs	
27103	5	AA042282	Hs.63481	ESTs	Weakly similar to kynurenine/alpha-aminoadipate aminotransferase [R.norvegicus]
17209	5	AA082933	EST - RC_AA082933	EST	
589	5	D50930	Hs.5084	Human mRNA for KIAA0140 gene complete cds	
17489	5	AA122394	Hs.70811	ESTs	
6293	5	X80878	Hs.95262	Human R kappa B mRNA complete cds	
5067	5	U77845	Hs.21254	Human hTRIP (hTRIP) mRNA complete cds	
23060	5	T23513	Hs.7147	ESTs	
28902	5	D80990	Hs.45247	ESTs	
32328	5	R76401	Hs.92262	ESTs	
33218	5	W70259	Hs.48523	ESTs	
28751	5	D45455	Hs.65524	ESTs	
21400	5	R19360	Hs.14651	ESTs	
15557	5	W36290	Hs.9115	ESTs	
12631	5	AA412293	Hs.21258	ESTs	
32282	5	R62578	Hs.62264	ESTs	
10416	5	AA006809	Hs.37589	ESTs	
40308	5	H96306	Hs.32960	Human mRNA for BST-1 complete cds	
11599	5	AA242829	Hs.7508	ESTs	
33220	5	W70279	Hs.94811	ESTs	Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]
23100	5	T23867	Hs.7316	ESTs	
15333	5	W24154	Hs.6166	ESTs	
8331	5	AA412556	EST - AA412556	EST	
9010	5	C01360	Hs.67384	Homo sapiens clone 23904 mRNA sequence	
4660	5	U53225	Hs.75283	Sortilin nexin 1	
25213	5	AA035444	Hs.100543	Homo sapiens clone 24505 mRNA sequence	
25242	5	AA039933	Hs.30941	Myasthenic syndrome antigen B [human fetal brain mRNA 3477 nt]	
28708	5	D20538	Hs.90165	EST	
7435	5	AA095412	Hs.26230	ESTs	
25538	5	AA095560	Hs.101442	ESTs	Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]
271	5	D14823	EST - D14823	EST	
5490	5	X04571	Hs.2230	Epidermal growth factor	
18812	5	F10040	Hs.13251	ESTs	
23393	5	T62918	Hs.11110	ESTs	Weakly similar to ZINC FINGER PROTEIN 42 [H.sapiens]
23446	5	T66282	Hs.12907	ESTs	
35204	5	AA399155	Hs.97600	ESTs	
31369	5	N67568	Hs.136395	ESTs	
5244	5	U85992	Hs.87187	Human clone IMAGE:35527 unknown protein mRNA partial cds	

FIGURE 7 (CONT.)

20835	5	N69215	Hs.37456	ESTs	
16502	5	AA027059	Hs.61425	EST	
23691	5	T87693	Hs.16414	ESTs	
31842	5	N90168	Hs.54593	EST	
7845	5	AA249611	EST - AA249611	ESTs	
29297	5	H65459	Hs.38323	ESTs	
7953	5	AA284403	Hs.74750	Homo sapiens mRNA for KIAA0554 protein partial cds	
36412	5	AA428464	Hs.98466	ESTs	
19357	5	H18929	EST - RC_H18929	ESTs	
16299	5	AA016258	EST - RC_AA016258	ESTs	
25312	5	AA047078	Hs.95278	ESTs Weakly similar to III ALU SUBFAMILY SO WARNING ENTRY III [H.sapiens]	
27617	5	AA448114	Hs.55409	ESTs	
42432	5	W46403	Hs.107293	ESTs	
38432	5	AA496983	Hs.78672	Laminin alpha 4	
32215	5	R45175	Hs.117183	ESTs	
15214	5	U93553	Hs.91310	Human alpha 1-antitrypsin transcription factor (hATF) mRNA complete cds	
15141	5	U78768	Hs.90957	Human TNF receptor associated factor 6 (TRAF6) mRNA complete cds	
20052	5	H97922	Hs.5376	Human LAR-interacting protein 1a mRNA complete cds	
7551	5	AA156838	Hs.107941	ESTs	
28451	5	AA259058	Hs.43516	ESTs	
42355	5	W20404	Hs.55405	ESTs	
39480	5	D60419	Hs.81915	STATMIN	
17369	5	AA101833	Hs.69293	EST	
14993	5	U22172	Hs.73046	Human DNA damage repair and recombination protein RAD52 pseudogene mRNA partial cds	
23400	5	T63336	Hs.105095	ESTs	
21153	5	R05315	EST - RC_R05315	ESTs	
14282	5	AA505141	EST - RC_R01081	ESTs	
21104	5	R01081	EST - RC_R01081	ESTs	
32825	5	W20364	Hs.55412	ESTs	
35018	5	AA346591	EST - RC_AA346591	ESTs	
25104	5	AA019599	Hs.103351	ESTs	
19235	5	H12725	Hs.31181	ESTs	
34079	5	AA347209	Hs.7841	Human mRNA for KIAA0324 gene partial cds	
21501	5	R26855	Hs.24120	ESTs	
18331	5	AA218543	Hs.10881	Homo sapiens mRNA for KIAA0541 protein partial cds	
37529	5	AA456112	Hs.99410	ESTs	
15532	5	W28844	Hs.5298	ESTs Highly similar to PUTATIVE 2-HYDROXYACID DEHYDROGENASE IN BISC-CSPA INTERGENIC REGION [Escherichia coli]	
11858	5	AA262308	Hs.106385	ESTs	
29450	5	H80865	Hs.11026	Phosphatidylinositol glycan class F	
37294	5	AA450127	Hs.110571	ESTs Highly similar to MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118 [Mus musculus]	

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FIGURE 7 (CONT.)

35170	5	AA397830	Hs.98347	ESTs Weakly similar to rnp-1 [H.sapiens]
23201	5	T40652	Hs.8279	ESTs
27012	5	AA308913	Hs.45231	ESTs
28767	5	D45808	Hs.83792	Surfactant pulmonary-associated protein D
17777	5	AA148634	Hs.62788	ESTs Weakly similar to hypothetical L1 protein [H.sapiens]
20588	5	N58009	Hs.38218	ESTs
20356	5	N39453	Hs.27371	ESTs
23375	5	T59570	Hs.10615	EST
17030	5	AA070188	EST - RC_AA070188	
30752	5	N52340	Hs.118084	EST
25808	5	AA149228	Hs.95821	Human osteoclast stimulating factor mRNA complete cds
31345	5	N87268	Hs.50139	ESTs
30784	5	N52857	Hs.47558	ESTs
13707	5	AA460281	Hs.14697	ESTs
25199	5	H25751	Hs.57082	EST
39003	4	AA609920	Hs.112785	EST
41529	4	R54458	Hs.2899	Glypican 1
3151	4	M83652	Hs.53155	Properdin P factor complement
33134	4	W61264	Hs.57829	ESTs
29186	4	H24458	Hs.85053	Homo sapiens clone 24440 mRNA sequence
12863	4	AA425782	Hs.27573	ESTs
11949	4	AA279827	Hs.125035	ESTs
31925	4	N92924	Hs.125032	ESTs
35258	4	AA398428	Hs.97628	ESTs
39538	4	H27216	Hs.107635	ESTs
30796	4	N53046	Hs.91148	ESTs Moderately similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]
19464	4	H24458	Hs.32085	EST
42486	4	W68410	Hs.106857	Calbindin 2 (29kD calretinin)
34274	4	AA236352	Hs.110821	ESTs
37848	4	AA459917	Hs.99506	EST
3169	4	M85085	Hs.693	Cleavage stimulation factor 3' pre-RNA subunit 2 64kD
10326	4	R96417	Hs.107795	ESTs
15063	4	U56814	Hs.88646	Homo sapiens DNase gamma mRNA complete cds
23571	4	T80628	Hs.108169	ESTs
14377	4	AA599583	Hs.15289	ESTs Weakly similar to HSM-2 [H.sapiens]
22255	4	R56239	Hs.6656	ESTs
36820	4	AA435968	Hs.98849	ESTs Weakly similar to thioraxoid [D.melanogaster]
35063	4	AA358015	Hs.99998	EST
12378	4	AA399271	Hs.19510	ESTs
31406	4	N88163	Hs.49455	EST

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FIGURE 7 (CONT.)

27430	4	AA429028	Hs.42678	ESTs Moderately similar to IIII ALU SUBFAMILY SB WARNING ENTRY IIII [H.sapiens]
30352	4	N40170	Hs.45046	ESTs
30599	4	N50039	Hs.47004	ESTs
27894	4	AA460319	Hs.48469	ESTs
31844	4	N90218	Hs.54607	ESTs
24935	4	AFEX	AFEX-HUNGAPDH/M33187_M	
40906	4	N68829	Hs.131510	ESTs
35220	4	AA398246	Hs.37594	ESTs
10024	4	N94832	Hs.121699	ESTs
4238	4	U33053	Hs.2409	Human lipid-activated protein kinase PRK1 mRNA complete cds
26558	4	AA256396	Hs.88156	EST
24716	4	Z38734	Hs.22550	ESTs
19243	4	II13539	Hs.31222	ESTs
41844	4	T15833	Hs.100227	EST
39774	4	H17948	Hs.106311	Homo sapiens DGS-A mRNA 3' end
20111	4	N21380	Hs.25497	H.sapiens mRNA for ROX protein
24008	4	T98337	Hs.18824	ESTs
8316	4	AA410529	Hs.30732	ESTs
35072	4	AA358738	EST - RC_AA358738	
39784	4	H21819	Hs.14896	Homo sapiens clone 24580 mRNA sequence
1517	4	J04501	Hs.772	Glycogen synthase 1 (muscle)
9164	4	D38081	Hs.89887	Thromboxane A2 receptor
35027	4	AA349998	Hs.96937	ESTs
35185	4	AA398015	Hs.97590	Unlabeled
25570	4	AA278425	Hs.85428	ESTs Weakly similar to hypothetical L1 protein [H.sapiens]
19759	4	H54352	Hs.36873	ESTs
34310	4	AA243416	Hs.75470	Homo sapiens mRNA expressed in osteoblast complete cds
39961	4	H57317	Hs.103161	ESTs
23249	4	T47919	Hs.8749	ESTs
19119	4	H09077	Hs.30895	EST
14158	4	AA480182	Hs.118598	ESTs
22866	4	R99338	Hs.36189	EST
16935	4	AA059392	Hs.66791	ESTs
41950	4	T33137	Hs.7967	ESTs
20404	4	N46594	Hs.30881	Homo sapiens liprin-alpha2 mRNA complete cds
18406	4	AA227962	Hs.112075	ESTs Weakly similar to reverse transcriptase [M.musculus]
16560	4	AA031308	Hs.24341	ESTs
26098	4	AA242831	Hs.87606	ESTs
34360	4	AA251547	Hs.104358	EST
16830	4	AA054222	Hs.40400	ESTs

FIGURE 7 (CONT.)

32668	4	T69284	Hs.2314	Mannose-binding lectin soluble (opsonic defect)
32912	4	W38051	EST - RC_W38051	
16230	4	AA011549	ESTs	
29696	4	H87909	ESTs	
8232	4	AA397529	EST - AA397529	
25584	4	AA112320	ESTs	
30878	4	N56892	ESTs	
40579	4	N34524	ESTs	
8026	4	AA301842	ESTs	ESTs Weakly similar to reverse transcriptase homolog [H.sapiens]
3094	4	N77481	ESTs	Human antigen (MAGE-1) gene complete cds
17480	4	AA121974	EST - RC_AA121974	
15766	4	W65777	ESTs	
34865	4	AA299903	ESTs	
29779	4	N20290	ESTs	
6547	4	X95808	ESTs	Human mRNA for KIAA0385 gene complete cds
24479	4	W96222	ESTs	
16135	4	AA004805	ESTs	Human Toll-like receptor 2 (TLR2) mRNA complete cds
11098	4	AA151243	ESTs	
14388	4	AA599742	ESTs	
36078	4	AA417275	ESTs	
23440	4	T65568	ESTs	
20863	4	N69989	ESTs	
20347	4	N39117	ESTs	
7795	4	AA247455	ESTs	
10729	4	AA054087	ESTs	
12734	4	AA419200	ESTs	
24446	4	W93119	ESTs	
30734	4	N52083	ESTs	
20841	4	N62353	ESTs	
21183	4	R06769	ESTs	
18138	4	AA192757	ESTs	
35310	4	AA398662	ESTs	
39497	4	D80154	ESTs	
29868	4	N22343	ESTs	
8707	4	AA479995	ESTs	Human mRNA for KIAA0583 protein partial cds
18472	4	AA233299	ESTs	
24720	4	Z39754	ESTs	
40825	4	N63923	ESTs	
15375	4	W26395	ESTs	
32869	4	W35211	ESTs	

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FIGURE 7 (CONT.)

4641	4	US2426	Hs.74597	Homo sapiens GOK (STIM1) mRNA complete cds
11786	4	AA258816	Hs.31707	ESTs
21571	4	R33841	Hs.24709	ESTs Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]
1600	4	K03474	EST - K03474	ESTs
21103	4	R01068	Hs.14603	ESTs
22993	4	T16358	Hs.108443	ESTs
38686	4	AA598661	Hs.103849	ESTs
27148	4	AA406231	Hs.100113	Human mRNA for KIAA0381 gene partial cds
26680	4	D20261	Hs.80067	ESTs
36397	4	AA426372	Hs.105804	Human mRNA for histone H1x complete cds
26915	4	AA330634	EST - RC_AA330634	ESTs
6912	4	Z35278	Hs.25336	Hsapiens PEBP2aC1 acute myeloid leukaemia mRNA
31825	4	N89848	Hs.54543	ESTs
10763	4	AA057620	Hs.30607	ESTs
17007	4	AA069696	Hs.67317	ESTs
33439	4	W88445	Hs.56844	ESTs
27657	4	AA447612	Hs.60435	ESTs
26288	4	AA253393	Hs.87734	ESTs
8235	4	AA397616	Hs.107245	ESTs Moderately similar to potassium channel protein Raw3 [R.norvegicus]
12114	4	AA287097	Hs.25114	ESTs
879	4	D88155	Hs.97196	Human steroidogenic factor 1 mRNA complete cds
30793	4	N52978	Hs.51919	Plasminogen-like protein
13522	4	AA454115	Hs.6000	ESTs
20819	4	N88730	Hs.12160	ESTs
20019	4	H94266	Hs.9451	ESTs
32396	4	R95778	Hs.93008	EST
38162	4	AA487165	Hs.105706	EST
8487	4	AA442669	EST - AA442669	ESTs
18444	4	AA232646	Hs.68061	ESTs
16183	4	AA010070	Hs.60339	EST
33047	4	W49755	Hs.89359	ESTs Moderately similar to type Ia hair keratin a3 [H.sapiens]
14797	4	S82769	Hs.104133	GABAA receptor gamma 3 subunit [human fetal brain mRNA Partial 1535 nt]
26107	3	AA243172	Hs.87619	ESTs
24421	3	W82001	Hs.120969	ESTs
27665	3	AA447759	Hs.134724	ESTs
19154	3	H10047	Hs.22515	ESTs
10833	3	AA121380	Hs.27567	ESTs Weakly similar to similar to alpha-13-mannosyl-glycoprotein beta-1 2-N-acetylglucosaminyltransferase [C.elegans]
7254	3	AA074897	EST - AA074897	ESTs
18684	3	F04262	Hs.22137	ESTs
40987	3	N77904	Hs.44380	ESTs

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FIGURE 7 (CONT.)

14971	3	U10493	Hs.438	Human Mox1 protein (MOX1) mRNA complete cds
11217	3	AA180487	Hs.62440	ESTs
16782	3	AA047265	Hs.82582	Homo sapiens mRNA for osteoblast specific cysteine-rich protein complete cds
21477	3	R26054	Hs.23531	ESTs
21382	3	R16896	Hs.89615	PROTEIN KINASE C THETA TYPE
19508	3	H28966		EST - RC_H28966
30301	3	N36174	Hs.2507	5-HYDROXYTRYPTAMINE 2B RECEPTOR
21553	3	R33005	Hs.23153	ESTs Weakly similar to ETX1 (alternatively spliced) [H.sapiens]
6102	3	X70340	Hs.2023	Transforming growth factor alpha
23502	3	T70580	Hs.13759	ESTs
8333	3	AA412620	Hs.4248	ESTs
30500	3	N46329	Hs.30490	ESTs Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]
21431	3	R22057	Hs.23336	ESTs
35920	3	AA412290	Hs.98124	ESTs
12065	3	AA283907	Hs.110480	Homo sapiens clone 23837 mRNA sequence
19156	3	H10068	Hs.25924	Homo sapiens clone 24468 mRNA sequence
24844	3	Z41301	Hs.23539	ESTs
33178	3	W68846	Hs.141719	EST
2052	3	L36618	Hs.75339	Inositol polyphosphate phosphatase-like protein 1 (51C protein)
15327	3	W23474	Hs.23352	ESTs
16874	3	F10565	Hs.12345	ESTs
9039	3	C02049	Hs.106291	ESTs
37470	3	AA454935	Hs.96568	ESTs
19167	3	H10841	Hs.22928	ESTs
34868	3	AA303078	Hs.94479	Human GT334 protein (GT334) gene mRNA complete cds
30591	3	N49952	Hs.138717	ESTs
26997	3	AA398468	Hs.93090	ESTs
18547	3	F03004	Hs.27109	ESTs
17867	3	AA157281	Hs.72183	ESTs
15280	3	W07019	Hs.35088	ESTs
20465	3	N51599	Hs.14633	ESTs
11047	3	AA142849	Hs.22660	ESTs
19451	3	H23747	Hs.31697	ESTs
41621	3	R69233	Hs.101504	ESTs
2822	3	M55621	Hs.117946	N-acetylglucosaminyltransferase I
28675	3	D20188	Hs.74876	ESTs
13928	3	AA478441	Hs.11590	ESTs
28473	3	H83694	Hs.40478	ESTs
25829	3	AA151621	Hs.110964	ESTs
28532	3	C20680	Hs.68513	EST

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FIGURE 7 (CONT.)

32376	3	R91391	Hs.64391	ESTs	
12064	3	AA283648	Hs.11387	ESTs	Weakly similar to KIAA0009 [H.sapiens]
15547	3	W32012	Hs.29353	ESTs	
40284	3	H95073	Hs.108734	ESTs	Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]
22881	3	R99595	Hs.36152	ESTs	
15525	3	W28763	Hs.16349	ESTs	Homo sapiens KIAA0431 mRNA partial cds
17968	3	AA167496	Hs.72695	EST	
3836	3	U12707	Hs.2157	EST	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
4528	3	U48251	Hs.75871	ESTs	Homo sapiens protein kinase C-binding protein RACK7 mRNA partial cds
29784	3	N20468	Hs.42849	ESTs	Weakly similar to line-1 protein ORF2 [H.sapiens]
7892	3	AA262100	Hs.133302	ESTs	EST - AA262100
15279	3	W05746	Hs.9225	ESTs	Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parastichopus porvimensis]
42064	3	T63364	Hs.20509	ESTs	
17943	3	AA165117	Hs.19520	ESTs	Sodium/potassium ATPase gamma subunit
4596	3	U50743	Hs.61148	ESTs	
16421	3	AA022541	Hs.105713	EST	EST - U87611
4014	3	U87611	Hs.2759	EST	Carilage linking protein 1
38171	3	AA487301	Hs.12575	ESTs	
20168	3	N24106	Hs.16511	ESTs	
18791	3	F09892	Hs.15769	ESTs	
24281	3	W79773	Hs.34421	ESTs	
13996	3	AA480907	Hs.99152	EST	
20583	3	N57797	Hs.23466	ESTs	
37181	3	AA448158	Hs.31597	ESTs	
21450	3	R23146	Hs.7898	EST	Homo sapiens clone 23938 mRNA sequence
19834	3	H44868	Hs.91797	ESTs	EST - Z96810
10163	3	R54534	Hs.92897	ESTs	Retinoblastoma-binding protein 1[alternative products]
7059	3	Z96810	Hs.8023	EST	EST - RC_F09302
25762	3	AA136066	Hs.30204	ESTs	Homo sapiens mRNA for SPDP
27426	3	AA428900	Hs.23523	ESTs	EST - X97748
29023	3	F03302	Hs.8135	ESTs	
10989	3	AA132366	Hs.97568	ESTs	
6587	3	X97748	Hs.112774	ESTs	
8722	3	AA481309	Hs.8944	ESTs	Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens]
21476	3	R26065	Hs.113619	ESTs	
14096	3	AA487568			
35392	3	AA399562			
28608	3	C21509			
13350	3	AA449297			
41202	3	R12808			

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FIGURE 7 (CONT.)

15612	3	W51955	Hs.73372	ESTs	
33930	3	AA169539	Hs.95870	ESTs	
34215	3	AA233855	Hs.104252	UTROPIIIN	
19208	3	H11734	Hs.110454	ESTs	Weakly similar to coded for by <i>C. elegans</i> cDNA cm10e3 [<i>C. elegans</i>]
24047	3	W15386	Hs.26750	ESTs	
14852	3	T52059	Hs.100383	ESTs	Highly similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [<i>Rattus norvegicus</i>]
27815	3	AA455370	Hs.59729	ESTs	
22610	3	R81173	Hs.11482	ESTs	Highly similar to F11 antigen [<i>H. sapiens</i>]
37510	3	AA455896	Hs.2699	Glypican 1	
37825	3	AA470073	Hs.104836	ESTs	
13321	3	AA448238	Hs.16714	ESTs	
25999	3	AA235375	Hs.87421	EST	
9738	3	M13150	Hs.99500	MAST oncogene	
16248	3	AA013125	Hs.40871	ESTs	
27582	3	AA442856	Hs.61979	ESTs	Moderately similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [<i>H. sapiens</i>]
16546	3	AA029452	Hs.95162	ESTs	
16981	3	AA064859	EST - RC_AA064859		
22128	3	R51021	Homo sapiens retinoic acid hydroxylase mRNA complete cds		
23312	3	T54617	EST - RC_T54617		
16783	3	F09741	Hs.124205	ESTs	
10308	3	R86920	Hs.127585	ESTs	
22518	3	R71892	Hs.25996	ESTs	Highly similar to 40S RIBOSOMAL PROTEIN S27A [<i>Homo sapiens</i> <i>Cavia porcellus</i>]
8255	3	AA400226	Hs.25024	ESTs	Weakly similar to estrogen-responsive finger protein efp [<i>H. sapiens</i>]
16361	3	AA019218	Hs.40550	ESTs	Moderately similar to proto-cadherin 3 [<i>R. norvegicus</i>]
5453	3	X02910	Hs.2037	Tumor necrosis factor	
22509	3	R71383	Hs.29190	ESTs	
20055	3	H98657	Hs.27291	ESTs	
31091	3	N63076	Hs.138746	EST	
39050	3	AA610112	Hs.124849	ESTs	
2493	3	M22919	Hs.77385	MYOSIN LIGHT CHAIN ALKALI SMOOTH-MUSCLE ISOFORM	
30159	3	N32623	Hs.44069	ESTs	
28913	3	F01580	Hs.22583	ESTs	Highly similar to co-repressor protein [<i>M. musculus</i>]
12257	3	AA350030	Hs.4221	ESTs	
359	3	D26350	Hs.75119	Human mRNA for type 2 inositol 145-bisphosphate receptor complete cds	
23587	3	T81356	Hs.14908	ESTs	
14323	3	AA598575	Hs.12851	ESTs	
27231	3	AA416936	Hs.7491	Homo sapiens methionine synthase reductase (MTRR) mRNA complete cds	
34814	3	AA338728	Hs.133096	ESTs	
21233	3	R08359	Hs.19308	ESTs	
22650	3	T86475	Hs.16193	ESTs	

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FIGURE 7 (CONT.)

14236	3	AA496891	Hs.5011	ESTs Weakly similar to The h1237 gene product is related to S.pombe rad21 gene product. [H.sapiens]
17617	3	AA131394	Hs.44572	ESTs Weakly similar to The KIAA0147 gene product is related to adenylyl cyclase. [H.sapiens]
24594	3	Z38804	Hs.22555	ESTs Highly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus]
7426	3	AA095895	Hs.111818	ESTs
34871	3	AA300151	Hs.125146	ESTs
17982	3	AA167051	Hs.83525	Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence
24337	3	W86007	Hs.8876	ESTs
22589	3	R79580	Hs.29874	ESTs
24554	3	Z30522	Hs.27082	EST
22348	3	R61750	Hs.6136	ESTs
30217	3	N94288	Hs.44554	EST
10210	3	R87468	Hs.131828	ESTs
22156	3	R52145	Hs.25894	ESTs
16404	3	AA021204	Hs.60554	ESTs Moderately similar to sodium-calcium exchanger form 3 [R.norvegicus]
29310	3	H66842	Hs.88729	ESTs
15956	3	Z21217	Hs.77695	Human mRNA for KIAA0008 gene complete cds
9758	3	M26393	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
20917	3	N72295	Hs.18004	ESTs
22964	3	U84573	EST - U84573	EST
9806	2	T10362	Hs.57358	ESTs
29007	2	M79462	Hs.89633	Probable transcription factor PML (alternative products)
39646	2	N21031	Hs.42630	ESTs
22733	2	H02255	Hs.7268	EST
22733	2	R92181	Hs.34558	EST
23233	2	T41177	Hs.8410	ESTs
18549	2	F01360	Hs.6092	ESTs Highly similar to HYPOTHETICAL 54.9 KD PROTEIN CO2F5.7 IN CHROMOSOME III [Caenorhabditis elegans]
31092	2	N91968	Hs.39635	ESTs
18661	2	F10452	Hs.12254	ESTs
24553	2	Z38521	Hs.9428	ESTs
19289	2	H16568	Hs.23748	ESTs
30723	2	AA480911	Hs.22393	ESTs
14185	2	N51935	Hs.47374	EST
34031	2	AA192514	Hs.83577	Human LIM protein MLP mRNA complete cds
18434	2	AA232206	Hs.50743	ESTs
14647	2	D20378	Hs.30731	EST
41048	2	N92734	Hs.115985	ESTs
38157	2	AA468558	Hs.105702	EST
33299	2	W73790	Hs.73803	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
16816	2	AA035446	Hs.81783	ESTs
3276	2	M93718	Hs.76983	Nitric oxide synthase 3 (endothelial cell)

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FIGURE 7 (CONT.)

33022	2	W46976	Hs.04667	EST	
31704	2	N75055	Hs.14632	ESTs	
38713	2	AA608577	Hs.112575	ESTs	
20396	2	N48293	Hs.12296	ESTs	
10310	2	R87373	Hs.75429	ESTs	
22388	2	R63895	Hs.1432	Protein Kinase C substrate 80K-H	
15936	2	Z11737	Hs.2664	Flavin-containing monooxygenase 4	
23667	2	T68826	Hs.142528	ESTs	
30903	2	N57730	Hs.48058	EST	
20938	2	N73988	Hs.37477	ESTs Weakly similar to No definition line found [C.elegans]	
5935	2	X62466	Hs.106338	CDW52 antigen (CAMPATH-1 antigen)	
19304	2	H16976	Hs.7973	ESTs	
8804	2	AB000463	Hs.16227	Homo sapiens mRNA for SH3 binding protein complete cds clone:RES4-23A	
41485	2	R49689	Hs.5260	ESTs Weakly similar to C08G8.3 [C.elegans]	
24685	2	Z39406	Hs.11797	ESTs Moderately similar to retinoid X receptor interacting protein [M.musculus]	
25403	2	AA063316	EST - RC_AA063316		
35773	2	AA406219	Hs.104747	ESTs	
27965	2	AA464287	Hs.24912	Homo sapiens bicuculal-D (BICD) mRNA complete cds	
16911	2	AA058658	Hs.60669	ESTs	
42315	2	T97353	EST - RC_T97353		
40632	2	N45221	EST - RC_N45221		
15722	2	W79046	Hs.15250	Homo sapiens DBI-related protein mRNA complete cds	
14842	2	T47519	EST - T47519		
36088	2	AA417344	Hs.98220	ESTs Moderately similar to located at OATL1 [H.sapiens]	
15527	2	W28788	Hs.63260	Phosphodiesterase 8A cGMP-specific rod alpha	
10302	2	R84933	Hs.133217	ESTs	
21243	2	R08773	Hs.20231	ESTs	
7759	2	AA234687	Hs.64147	ESTs Weakly similar to F59C6.4 [C.elegans]	
31872	2	N74336	Hs.91681	ESTs	
26799	2	AA284722	Hs.89121	ESTs	
25857	2	AA156504	Hs.95875	EST	
16695	2	AA043115	Hs.9452	ESTs Weakly similar to ORF YDL077c [S.cerevisiae]	
964	2	HG1804	EST - HG1804-HT1829		
12439	2	AA401452	Hs.32060	ESTs	
18999	2	H41235	Hs.109968	ESTs	
24223	2	W70158	Hs.28698	ESTs	
21052	2	N93764	Hs.10175	ESTs Weakly similar to hypothetical protein [H.sapiens]	
17463	2	AA121338	EST - RC_AA121338		
28949	2	F03032	Hs.65823	ESTs Weakly similar to reverse transcriptase homolog [H.sapiens]	
34140	2	AA215637	Hs.104188	ESTs	

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FIGURE 7 (CONT.)

7465	2	AA120886	EST - AA120886	
17376	2	AA102425	EST - RC_AA102425	
5130	2	U79288	Hs.85953	Homo sapiens clone 24440 mRNA sequence
30041	2	N27628	Hs.132744	Homo sapiens clone 24525 mRNA sequence
10684	2	H48488	Hs.143798	ESTs
8165	2	AA359093	EST - AA359093	
19202	2	H11509	Hs.22482	ESTs
20439	2	N50785	Hs.13269	ESTs
10431	2	AA011310	Hs.3757	ESTs
29707	2	H98244	Hs.42519	ESTs
39868	2	H37909	Hs.107680	ESTs
8988	2	C00185	Hs.10444	ESTs
41350	2	R40442	Hs.75952	Glutathione S-transferase M5
13121	2	AA436156	Hs.110837	ESTs
15747	2	W86550	Hs.132188	ESTs
18674	2	F03989	Hs.18995	ESTs Weakly similar to KIAA0412 [H.sapiens]
914	2	HG1019	EST - HG1019-HT1019	
23804	2	T91086	EST - RC_T91086	
26556	2	AA276089	Hs.88550	ESTs
8567	2	AA453381	Hs.104900	ESTs
30457	2	N47685	Hs.64607	Human RACH1 (RACH1) mRNA complete cds
21975	2	R45441	Hs.23710	ESTs
17452	2	AA120766	Hs.70724	ESTs
31958	2	N93495	Hs.54950	ESTs
31495	2	N98850	Hs.49759	ESTs
32490	2	T16389	Hs.81248	Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA complete cds
39174	2	AA621067	Hs.112944	ESTs
21572	2	R34073	Hs.89740	Zinc finger protein 136 (clone pHZ-20)
15914	2	Y09046	Hs.81972	V-akt avian sarcoma viral oncogene homolog
12014	2	AA281769	Hs.7214	Human Hpast (IPAST) mRNA complete cds
39777	2	H18412	Hs.75253	Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA alternatively spliced partial cds
9484	2	H50178	Hs.108081	ESTs Highly similar to PROTEIN PHOSPHATASE PP2A 55 KD REGULATORY SUBUNIT NEURONAL ISOFORM [Oryzotagus curticulus]
19147	2	H09751	Hs.117619	ESTs
36276	2	AA424179	Hs.124027	ESTs
16475	2	AA025903	Hs.57911	ESTs
21304	2	R11208	Hs.20755	ESTs
11199	2	AA176446	Hs.10024	ESTs
18093	2	AA187955	Hs.85564	ESTs
19190	2	H11274	Hs.31040	EST
15710	2	W76399	EST - W76399	

FIGURE 7 (CONT.)

18707	2	F04627	Hs.23540	ESTs	
6477	2	X91504	Hs.64904	Transcription factor COUP 2 (a.k.a. ARP1)	
20823	2	N68869	Hs.15118	ESTs	
16336	2	AA018901	Hs.75949	EXTRACELLULAR SIGNAL-REGULATED KINASE 3	
19680	2	H48457	Hs.35104	ESTs	
24833	2	Z41087	Hs.19066	ESTs	
24058	2	W23709	Hs.109047	ESTs	
28180	2	AA251230	Hs.112272	ESTs	
37177	2	AA47988	Hs.7765	ESTs	
14047	2	AA482597	Hs.26054	ESTs	
10770	2	AA059683	Hs.22552	ESTs	
41094	2	T47601	Hs.138805	ESTs	
19217	2	I112243	EST - RC_H12243		
36532	2	AA429889	Hs.68882	Acrocin	
23378	2	T60072	Hs.10688	ESTs	
1450	2	J03071	Hs.115352	Growth hormone 1	
8007	2	AA293072	Hs.97283	ESTs Moderately similar to IIII ALU CLASS B WARNING ENTRY IIII [H.sapiens]	
17266	2	AA084723	Hs.24812	ESTs	
24819	2	Z40923	Hs.89491	DNA-BINDING PROTEIN A	
6532	2	X95325	Hs.86641	ESTs	
26850	2	AA287851	Hs.108788	ESTs	
34175	2	AA227523	Hs.108788	ESTs	
34620	2	AA282169	EST - RC_AA282169		
27085	2	AA402495	Hs.77978	ESTs	
20173	2	N24730	Hs.15420	ESTs	
17574	2	AA129060	EST - RC_AA129060		
22330	2	T60920	Hs.26419	Homo sapiens clone 24510 mRNA sequence	
30070	2	N28698	Hs.44076	EST	
20487	2	N52322	Hs.19978	ESTs	
724	2	D83703	Hs.30729	Peroxisomal biogenesis factor 6	
4132	2	U27655	Hs.82294	Human RGP3 mRNA complete cds	
8557	2	AA432705	Hs.23954	ESTs Weakly similar to D2045.9 [C.elegans]	
33659	2	W85628	Hs.59718	EST	
13375	2	AA449716	Hs.5723	ESTs	
30891	2	N57007	Hs.94074	EST	
13988	2	AA480045	Hs.7934	ESTs	
22308	2	R59906	Hs.100530	ESTs	
23167	2	T33184	Hs.12840	Homo sapiens germline mRNA sequence	
20873	2	N70134	Hs.31476	ESTs	
7231	2	AA059327	Hs.6580	Homo sapiens clone 23718 mRNA sequence	

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FIGURE 7 (CONT.)

24582	2	Z38752	Hs.28530	ESTs	
11320	2	AA213867	Hs.22222	ESTs	
16388	2	AA020781	Hs.60847	ESTs	
24608	2	Z38888	Hs.25046	ESTs	
7809	2	AA248085	Hs.12469	Homo sapiens clone 23930 mRNA sequence	
13163	2	AA437225	Hs.22410	ESTs	
20549	2	N54991	Hs.37581	ESTs	
1139	2	HG3227-	ESTs	Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]	
35572	2	AA041489	EST - HG3227-HT3404		
6964	2	Z49105	Hs.137591	EST - RC_AA401489	
27704	2	AA449704	Hs.77637	H.sapiens HD21 mRNA	
33196	2	W69725	Hs.10711	Homo box A4	
30963	2	N59373	Hs.26612	ESTs	
13888	2	AA476937	Hs.24441	ESTs	
16164	2	AA007509	Hs.75395	Human mRNA for TPRD complete cds	
18083	2	AA181928	Hs.70954	Homo sapiens mRNA for hoxA7 protein	
20107	2	N21207	Hs.129942	ESTs Moderately similar to RETROVIRUS-RELATED POLYPROTEIN [Mus musculus]	
23004	2	T16556	Hs.6053	ESTs	
16238	2	AA011678	Hs.40470	ESTs	
18189	2	AA195042	Hs.85978	ESTs	
37567	2	AA457377	EST - RC_AA457377		
2174	2	L42611	Hs.11759	KERATIN TYPE II CYTOSKELETAL 6D	
38958	2	AA609707	Hs.112751	ESTs	
37919	2	AA478162	Hs.104965	ESTs	
28905	2	D81123	Hs.57475	ESTs	
33315	2	W74418	Hs.55410	ESTs	
7421	2	AA095600	EST - AA095600		
3745	2	I108117	Hs.80778	Human phospholipase c delta 1 mRNA complete cds	
19545	2	H37834	Hs.32699	ESTs	
21204	2	R07632	Hs.17949	ESTs	
8416	2	AA428531	EST - AA428531		
17589	2	AA128926	EST - RC_AA128926		
19572	2	H39195	Hs.22223	ESTs	
22760	2	R93714	Hs.33833	ESTs Highly similar to ALPHA-2-MACROGLOBULIN PRECURSOR [Homo sapiens]	
19354	2	H18829	Hs.121515	ESTs	
40618	2	N39565	Hs.108540	ESTs	
20913	2	N23708	Hs.43429	ESTs	
22571	2	R78565	Hs.138395	EST	
7598	2	AA174185	Hs.33354	Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA complete cds	
25385	2	AA059099	Hs.109727	ESTs	

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FIGURE 7 (CONT.)

14176	2	AA490620	Hs.11809	ESTs	
37400	2	AA453578	Hs.120994	ESTs	Weakly similar to T20D3.5 [C.elegans]
29487	2	H85120	Hs.80881	N-ACETYLACTOSAMINE SYNTHASE	
10197	2	R64199	Hs.50785	Homo sapiens vesicle trafficking protein sec22b mRNA complete cds	
322	2	D21241		EST - D21241_xpt1	
22224	2	R55192	Hs.25699	ESTs	
19488	2	H27675	Hs.25604	ESTs	
10568	2	AA029703	Hs.36574	ESTs	
10872	2	AA099357	Hs.15780	ESTs	Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]
29987	2	N26172	Hs.43760	ESTs	
30799	2	N53143	Hs.64001	ESTs	
9638	2	L07592	Hs.106415	Human peroxisome proliferator activated receptor mRNA complete cds	
21069	2	N98461	Hs.17706	ESTs	
27195	2	AA411473	Hs.65311	ESTs	
9241	2	D79565		EST - D79565	
9218	2	D81469	Hs.58896	ESTs	
22238	2	R55763	Hs.107287	ESTs	
7512	2	AA136389		EST - AA136389	
17438	2	AA115508	Hs.2780	Jun D proto-oncogene	
24932	2	AFX-		AFX-HSAC07X00351_M	
28911	2	F01525	Hs.3786	Gluamate receptor metabotropic 3	
10944	2	AA125969	Hs.34769	ESTs	Weakly similar to F35G12.9 [C.elegans]
42324	2	T98199	Hs.142702	ESTs	
34756	2	AA287665	Hs.0245	ESTs	
12743	2	AA421050	Hs.24545	ESTs	
21275	2	R10075	Hs.14890	ESTs	
13876	2	AA459389	Hs.26350	Homo sapiens mRNA for tyrosyl sulfotransferase-2	
13009	2	AA430474	Hs.16466	ESTs	
7403	2	AA094921	Hs.79788	ESTs	
11151	2	AA159961	Hs.25819	ESTs	
35669	2	AA404707	Hs.54865	ESTs	
17701	2	AA135941	Hs.71626	ESTs	
18713	2	F04686	Hs.21782	ESTs	
24144	2	W52312	Hs.30303	ESTs	Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]
30741	2	N52175	Hs.22222	ESTs	
23042	2	T23433	Hs.7105	ESTs	
18479	2	AA233483	Hs.87159	ESTs	
8314	2	AA410355	Hs.103081	ESTs	Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]
7990	2	AA291786	Hs.32822	ESTs	Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
10388	2	AA005355		EST - RC_AA005355	

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FIGURE 7 (CONT.)

9407	2	H20086	EST - H20086	
42791	2	AFX-	AFX-HUNGAPDH3197_M	
26302	2	AA255470	ESTs	
20722	1	N51924	Hs.88040	
24865	1	AFX-	Hs.47370	
38850	1	AA609262	AFX-Lyx-5	
13748	1	AA461300	EST - RC_AA609262	
6893	1	Z30843	ESTs	
31403	1	N68117	Hs.123123	Hsapiens mRNA for chloride channel (putative) 2139bp
17830	1	AA152312	Hs.41119	ESTs
10683	1	AA033874	Hs.72047	ESTs
20913	1	N72116	Hs.12035	ESTs
35607	1	AA402267	Hs.57435	Natural resistance-associated macrophage protein 2
9920	1	N44758	Hs.133475	ESTs Weakly similar to zinc finger protein [H.sapiens]
9468	1	H46074	Hs.141935	ESTs Weakly similar to transformation-related protein [H.sapiens]
29469	1	H82929	Hs.31562	ESTs
18121	1	AA191310	EST - RC_H82929	EST - RC_H82929
14705	1	D59382	AA191310	Protein phosphatase 2 (formerly 2A) regulatory subunit A (PR 65) beta isoform
16543	1	F04444	ESTs	EST - RC_D59382
16359	1	AA029430	Hs.61557	ESTs
40818	1	AA019197	Hs.40753	ESTs
35205	1	N63772	Hs.144550	Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-4.1. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydro
17794	1	AA398161	Hs.97602	ESTs
11347	1	AA249175	Hs.96334	ESTs Weakly similar to GOLIATH PROTEIN [Drosophila melanogaster]
17919	1	AA161125	Hs.72062	EST
22184	1	AA224245	Hs.26612	ESTs
14827	1	R53520	Hs.102755	ESTs
28091	1	T35288	Hs.80421	ESTs
28615	1	AA481788	Hs.87593	ESTs
17813	1	D59267	Hs.56782	ESTs
24655	1	AA151480	Hs.91202	ESTs
15611	1	Z39191	Hs.27282	ESTs Weakly similar to Lph17p [S.cerevisiae]
39598	1	H62865	Hs.35098	ESTs
15700	1	W73859	Hs.38132	ESTs
22045	1	R46965	Hs.78081	Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds
36770	1	AA435753	Hs.24796	EST
9877	1	N31127	EST - RC_AA435753	EST - RC_AA435753
22467	1	R68284	Hs.40098	ESTs
			Hs.28399	ESTs

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FIGURE 7 (CONT.)

32400	1	R97176	Hs.110783	ESTs	
10802	1	AA069425	Hs.20573	ESTs	
23033	1	T17353	Hs.106894	Homo sapiens clone 23918 mRNA sequence	
17563	1	AA129856	EST - RC_AA129856		
14867	1	T58588	Hs.100419	ESTs	
20266	1	N32118	Hs.107365	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]	
14447	1	AA609045	Hs.11759	ESTs	
37994	1	AA479819	EST - RC_AA479819		
12892	1	AA426521	Hs.18528	Homo sapiens mRNA for NA14 protein	
11970	1	AA280687	Hs.4069	ESTs	
19738	1	H53059	Hs.15548	ESTs	
14471	1	AA609346	Hs.20102	ESTs	
14855	1	T54762	Hs.9786	ESTs	
24725	1	Z39781	Hs.8004	Homo sapiens Duo mRNA complete cds	
5796	1	X55019	Hs.99975	Cholinergic receptor nicotinic delta polypeptide	
20259	1	N31598	Hs.12727	ESTs	
18441	1	AA232508	Hs.77480	ESTs	
18468	1	AA233177	Hs.87134	ESTs	
10164	1	R54743	Hs.19400	ESTs Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]	
8830	1	AB002319	Hs.8663	Human mRNA for KIAA0321 gene partial cds	
15287	1	W07461	Hs.121559	ESTs Highly similar to DIPHTHINE SYNTHASE [Saccharomyces cerevisiae]	
16477	1	AA028031	Hs.61312	ESTs	
21969	1	R45334	Hs.21175	ESTs	
22340	1	R61522	Hs.26892	ESTs	
12884	1	AA426259	EST - RC_AA426259		
8682	1	AA477891	Hs.104478	ESTs	
22594	1	R78793	Hs.25900	ESTs	
19131	1	H09331	Hs.122791	ESTs	
17103	1	AA074997	EST - RC_AA074997		
35620	1	AA402493	Hs.10552	ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus]	
35401	1	AA399593	Hs.97682	EST	
10901	1	AA112307	Hs.25224	ESTs	
19546	1	H37901	Hs.32706	ESTs	
15378	1	W26448	Hs.15071	ESTs Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]	
30292	1	N35978	Hs.82384	ESTs	
39087	1	AA620607	Hs.111591	ESTs	
37896	1	AA477463	Hs.77039	Ribosomal protein S28	
8836	1	AB002325	Hs.105917	Human mRNA for KIAA0327 protein complete cds	
18150	1	AA005428	Hs.60140	ESTs	
23955	1	T97467	Hs.18085	ESTs Weakly similar to alternatively spliced product using exon 13A [H.sapiens]	

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FIGURE 7 (CONT.)

37812	1	AA469939	Hs.105323	ESTs	
14782	1	S72370	Hs.89890	Pyruvate carboxylase	
23540	1	T79178	Hs.14463	ESTs	
41552	1	R59352	Hs.101253	Human mRNA for KIAA0296 gene complete cds	
21836	1	R42569	Hs.22444	EST	
11467	1	AA234089	Is.14593	ESTs	
18347	1	AA219230	Hs.86815	ESTs	
8215	1	AA389673	Hs.84344	ESTs Weakly similar to No definition line found [C.elegans]	
13505	1	W28366	Hs.7252	Human sapiens clone 24800 mRNA sequence	
22764	1	R93802	Hs.33687	ESTs	
14966	1	U07620	Hs.89661	Human MAP kinase mRNA complete cds	
24213	1	W69184	Hs.23973	ESTs	
8165	1	AA358888	Hs.104135	Human sapiens mRNA for DRIM protein	
32724	1	T90750	Hs.15230	ESTs Weakly similar to F25H2.2 [C.elegans]	
8212	1	AA388236	Hs.96757	Human sapiens transcription factor SUPT3H (SUPT3H) mRNA complete cds	
9834	1	M92269	Hs.22554	Homeo box B5 (2.1 protein)	
7229	1	AA059213	Hs.91898	ESTs	
15649	1	W58725	Hs.75074	H.sapiens mRNA for MAP kinase activated protein kinase	
42306	1	T96538	Hs.45080	Human K+ channel beta 1a subunit mRNA alternatively spliced complete cds	
9159	1	D31483	Hs.90062	Human sapiens clone 23565 unknown mRNA partial cds	
20040	1	H96712	Is.125198	ESTs	
42218	1	T86444	Hs.110095	ESTs	
15526	1	W28790	Hs.8124	ESTs	
17190	1	AA150182	Hs.42262	ESTs Weakly similar to HYPOTHETICAL 88.1 KO PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans]	
17595	1	AA129529	Hs.71165	EST	
31314	1	N68866	Hs.49278	EST	
9777	1	M57888	Hs.95946	GRANZYME H PRECURSOR	
15373	1	W26376	Hs.74563	THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR	
23547	1	T79448	Hs.14577	EST	
12076	1	AA284362	Hs.8448	ESTs Weakly similar to No definition line found [C.elegans]	
11956	1	AA279991	Hs.124691	ESTs	
15391	1	W26651	Hs.15961	ESTs	
9287	1	D82557	Hs.18104	ESTs	
16419	1	AA022466	Hs.81141	EST	
21713	1	R39930	Hs.21034	ESTs	
12805	1	AA427537	Hs.32419	ESTs	
30257	1	N34961	Hs.75673	H.sapiens mRNA for Zyxin	
28134	1	AA487622	Hs.64095	ESTs	
16380	1	AA019750	Hs.40787	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]	
10553	1	AA028904	Hs.33215	ESTs	

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FIGURE 7 (CONT.)

18053	1	AA180054	Hs.73677	ESTs	
39820	1	H24085	Hs.25443	ESTs	
7374	1	AA033378	Hs.101810	ESTs	
13109	1	AA435838	Hs.7985	ESTs	
19378	1	H19873	Hs.31670	ESTs	
24325	1	W84733	Hs.3978	ESTs	
22316	1	R60224	Hs.7065	ESTs	
24249	1	W73069	Hs.12600	ESTs	
16514	1	AA027948	Hs.44608	ESTs	
21421	1	R21741	Hs.23258	EST	
8397	1	AA426178	Hs.71725	ESTs	Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]
8412	1	AA428090	Hs.26102	ESTs	
10072	1	R14782	Hs.31931	ESTs	
10348	1	AA001908	Hs.18160	ESTs	
14492	1	AA009635	Hs.27497	ESTs	
14930	1	T92512	EST - T92512	EST	
15661	1	X81001	Hs.141503	Small inducible cytokine A5 (RANTES)	
16706	1	AA043800	Hs.62645	ESTs	
16744	1	AA045643	Hs.62868	EST	
16950	1	AA062980	Hs.65960	ESTs	
17836	1	AA155779	Hs.29759	ESTs	Weakly similar to IIII ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]
18834	1	F10207	Hs.13269	ESTs	
19178	1	H10992	Hs.100910	EST	
19767	1	H54720	Hs.36941	ESTs	
21341	1	R14959	Hs.21871	EST	Moderately similar to ninein [M.musculus]
21466	1	R24518	Hs.23674	EST	
21602	1	R36624	Hs.135137	ESTs	
21748	1	R40697	Hs.21250	EST	
21860	1	R43089	EST - RC_R43089	EST	
21891	1	R43590	Hs.13280	ESTs	
21937	1	R44508	Hs.22653	ESTs	
22006	1	R46244	Hs.23110	ESTs	
22054	1	R49116	Hs.25067	EST	
22222	1	R55042	Hs.105645	ESTs	
22292	1	R59335	Hs.141053	Homo sapiens bastrophin (VMP2) mRNA alternatively spliced product complete cds	
22383	1	R63463	Hs.23282	ESTs	
22446	1	R67259	Hs.25968	EST	
23103	1	T23939	Hs.7344	ESTs	
23972	1	T94562	Hs.17338	EST	
24291	1	W80642	Hs.16951	ESTs	

FIGURE 7 (CONT.)

24640	1	Z39086	Hs.21403	ESTs	
27519	1	AA435635	Hs.90695	ESTs	
32067	1	R06424	Hs.64896	ESTs	
32204	1	R44210	Hs.31440	EST	
32692	1	T79942	Hs.90330	ESTs	
33714	1	Z39430	Hs.65749	ESTs	
33733	1	Z39668	Hs.65792	ESTs	
33873	1	AFX-	AFX-DapX-3		
35434	1	AA400034	Hs.97760	EST	
35950	1	AA412498	Hs.104778	ESTs	
36483	1	AA428885	Hs.98563	EST	
36615	1	AA431469	Hs.98737	ESTs	
37329	1	AA452138	Hs.3781	Homo sapiens BAC clone RG118D07 from Tq31	
37700	1	AA461090	Hs.124826	EST	
38285	1	AA489940	Hs.105302	ESTs	
38887	1	AA500422	Hs.112705	EST	
38933	1	AA606608	Hs.112732	ESTs	
39894	1	H42037	Hs.144150	ESTs	
40244	1	H91660	Hs.30250	Homo sapiens short form transcription factor C-MAF (c-maf) mRNA complete cds	
40645	1	N47652	Hs.102624	EST	
40819	1	N63787	Hs.103304	ESTs	
41445	1	R45611	Hs.137699	ESTs	Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]
41700	1	R85829	Hs.101863	EST	
41776	1	T03170	Hs.100165	EST	
13254	1	AA446587	Hs.6775	ESTs	Highly similar to ALANINE AMINOTRANSFERASE [Homo sapiens]
8171	1	AA382708	Hs.5009	ESTs	Weakly similar to mTERF [H.sapiens]
23030	1	T17291	Hs.6995	ESTs	
8406	1	AA427510	Hs.104287	ESTs	
16767	1	AA046650	Hs.40342	ESTs	
25010	1	AA005315	Hs.51282	ESTs	
14629	1	T35529	EST - T35529		
34584	1	AA280934	Hs.132872	ESTs	Moderately similar to IIII ALU SUBFAMILY SC WARNING ENTRY IIII [H.sapiens]
15909	1	Y07868	Hs.38842	H.sapiens mRNA for Pltn isolate 1	
9922	1	N44971	Hs.107164	Specifin beta non-erythrocytic 1	
15381	1	W25450	Hs.107725	ESTs	Weakly similar to LIS-1 protein [H.sapiens]
22168	1	R53024	Hs.25985	ESTs	
11690	1	AA252782	Hs.31235	ESTs	
22959	1	T16510	Hs.6624	ESTs	
24490	1	Z38153	Hs.26921	ESTs	
19993	1	H91255	Hs.15227	ESTs	

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FIGURE 7 (CONT.)

19689	1	H48825	Hs.36291	ESTs	
12450	1	AA01809	Hs.19855	ESTs	
24368	1	W87280	Hs.124800	ESTs	
22565	1	R77631	Hs.29126	ESTs	
18872	1	F10542	Hs.12292	ESTs	
15358	1	W26105	Hs.8961	ESTs	
24186	1	W61319	Hs.37482	ESTs	Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]
23863	1	T93870	Hs.17265	ESTs	
23846	1	T93078	Hs.17117	EST	
15143	1	U79257	Hs.65921	Human clone 23932 mRNA sequence	
9711	1	L44334	Hs.10432	ESTs	Weakly similar to BENOMYL/METHOTREXATE RESISTANCE PROTEIN [Candida albicans]
22544	1	R74235	Hs.80844	Homo sapiens mRNA for KIAA0573 protein partial cds	
41506	1	R52088	EST - RC_H52088	EST - RC_H52088	
39345	1	C21105	Hs.7768	Homo sapiens FGF-1 intracellular binding protein (FIDP) mRNA complete cds	
22272	1	R58922	Hs.26590	ESTs	
16434	1	AA024494	Hs.81199	ESTs	
17255	1	AA084412	EST - RC_AA084412	EST - RC_AA084412	
22692	1	R88711	Hs.34183	ESTs	
38830	1	AA609189	Hs.116415	ESTs	
9179	1	D50312	Hs.102308	Human mRNA for uKATP-1 complete cds	
42547	1	W73946	EST - RC_W73946	EST - RC_W73946	
36195	1	AA421144	EST - RC_AA421144	EST - RC_AA421144	
29355	1	H70121	Hs.79592	ESTs	
34608	1	AA281765	Hs.104441	ESTs	
20779	1	N67553	Hs.16917	ESTs	
11081	1	AA149826	Hs.34274	ESTs	
12151	1	AA291269	Hs.24642	ESTs	
39335	1	H52379	EST - RC_H52379	EST - RC_H52379	
7157	1	AA037199	Hs.9699	ESTs	
17858	1	AA156596	Hs.72146	ESTs	
34985	1	AA302831	Hs.57732	Homo sapiens p38beta2 MAP kinase mRNA complete cds	
16445	1	AA232648	Hs.87068	ESTs	
22524	1	R72597	EST - RC_R72597	EST - RC_R72597	
19224	1	H12448	Hs.124570	ESTs	Weakly similar to unknown protein [H.sapiens]
18803	1	F09888	Hs.5244	ESTs	
13810	1	AA454669	Hs.23294	ESTs	Weakly similar to weak similarity to HSP90 [C.elegans]
18070	1	AA180352	Hs.72733	ESTs	
17937	1	AA164750	Hs.72489	ESTs	
39115	1	AA620735	Hs.112893	EST	
22517	1	R71892	Hs.25996	ESTs	Highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Cavia porcellus]

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FIGURE 7 (CONT.)

16906	1	AA058555	Hs.63392	EST	
14251	1	AA07049	Hs.32501	ESTs	
23923	1	T96407	Hs.17812	ESTs	
21177	1	R08569	Hs.19721	ESTs	
25705	1	AA131921	Hs.71030	ESTs	
18805	1	H57725	Hs.124031	ESTs	
19008	1	H47656	Hs.33991	EST	
36693	1	AA432389	Hs.98702	ESTs	
14036	1	AA482107	Hs.5473	ESTs	
20859	1	N68825	Hs.16762	ESTs	
23949	1	T93113	EST - RC_T93113		
18265	1	AA207122	Hs.85316	ESTs	
35275	1	AA398530	Hs.97363	ESTs	
10262	1	R77869	Hs.110493	ESTs	
21757	1	R40789	Hs.21299	ESTs	
21541	1	R31607	Hs.24420	ESTs	
16873	1	AA056258	Hs.63264	EST	
19846	1	H46008	Hs.31677	ESTs	
23719	1	T89160	Hs.138506	ESTs	
19508	1	H41581	Hs.31582	ESTs	Moderately similar to HYPOTHETICAL 58.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]
17382	1	AA102731	Hs.109072	ESTs	
16864	1	AA055871	Hs.63238	ESTs	
10897	1	AA111881	Hs.9192	ESTs	
17028	1	AA070178	EST - RC_AA070178		
19220	1	H12318	Hs.24324	ESTs	
9726	1	L44574	Hs.125235	ESTs	
24570	0	Z38681	Hs.27150	ESTs	
22167	0	R53021	Hs.25873	ESTs	
42537	0	W73417	Hs.103183	EST	
18806	0	F10005	Hs.12559	ESTs	
16585	0	AA033948	Hs.4236	ESTs	
17309	0	AA086232	Hs.68717	EST	Moderately similar to mariner transposase [H.sapiens]
22813	0	R97419	Hs.35718	ESTs	
18429	0	AA022953	Hs.61172	EST	
22013	0	R46526	Hs.25377	EST	
8409	0	AA431277	Hs.32419	ESTs	
22834	0	T10042	Hs.4205	ESTs	
13063	0	AA432385	Hs.1191	Human mRNA for KIAA0073 gene partial cds	
10122	0	R31745	EST - R31745		
18185	0	AA195263	Hs.85001	EST	

FIGURE 7 (CONT.)

33249	0	W72557	Hs.57836	ESTs
16966	0	AA063378	Hs.144270	ESTs
16363	0	AA223929	Hs.89902	EST
34154	0	AA219304	Hs.74581	ALPHA-2-MACROGLOBULIN PRECURSOR
16222	0	AA011210	Hs.85044	ESTs
17174	0	AA079306	EST - RC_AA079306	

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Primary Key	fold upregulated of Tumor over normal colon	Accession	Unigene Descriptor	CRF structural info
16074	>10	AA001507	ESTs	other
25047	>10	AA011031	ESTs	other
25082	>10	AA017257	ESTs	other
16490	>10	AA026418	ESTs	other
25179	>10	AA031268	H. sapiens mRNA for kinesin-2	other
25215	>10	AA035540	APOLIPOPROTEIN AI REGULATORY PROTEIN-1	other
25282	>10	AA044825	ESTs	other
16810	>10	AA053636	ESTs	other
16835	>10	AA054438	ESTs	SS.
10747	>10	AA055841	ESTs	other
10748	>10	AA055892	ESTs	other
16993	>10	AA065300	Human mRNA for KIAA0035 gene partial cds	other
17051	>10	AA070801	ESTs	TM
10840	>10	AA084104	ESTs	other
7296	>10	AA085661	ESTs	other
7325	>10	AA090842	ESTs Weakly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME 1 [Schizosaccharomyces pombe]	other
17419	>10	AA113349	EST	?
17541	>10	AA127458	ESTs	other
17559	>10	AA128407	ESTs	other
25669	>10	AA128978	ESTs	?
17600	>10	AA130596	ESTs	other
10992	>10	AA132523	Human sapiens BAC clone RG119C02 from 7p15	other
17654	>10	AA133250	ESTs	TM
17734	>10	AA137246	ESTs	other
25801	>10	AA148530	EST - RC_AA148530	TM
25836	>10	AA149007	EST	?
11121	>10	AA156359	Human TAR DNA-binding protein-43 mRNA complete cds	?
11160	>10	AA164289	ESTs	other
25925	>10	AA164494	ESTs Weakly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 [H. sapiens]	other
25934	>10	AA165355	Human clone cds unknown protein mRNA complete cds	?
17687	>10	AA169379	ESTs	other
18008	>10	AA171865	Human sapiens clone 24749 and 24750 mRNA sequences	TM
33953	>10	AA173200	Human HOKA1 mRNA long transcript and alternatively spliced forms complete cds	other
33980	>10	AA180223	CAMP-DEPENDENT PROTEIN KINASE TYPE II- ALPHA REGULATORY CHAIN	other
34013	>10	AA180888	EST - RC_AA180888	other
34014	>10	AA191348	ESTs	other
34015	>10	AA191353	ESTs	TM
34070	>10	AA198549	ESTs	other
18290	>10	AA206601	ESTs	?
34105	>10	AA207123	ESTs	SS.
34107	>10	AA209469	ESTs	other
18330	>10	AA216722	Human mRNA for apolipoprotein E receptor 2 complete cds	TM
18362	>10	AA223912	Ribonuclease L (2'5'-oligoadenylate synthetase- dependent) inhibitor	other
18392	>10	AA227751	ESTs	SS.
34188	>10	AA228030	ESTs	TM
34197	>10	AA232315	Human sapiens clone 23797 and 23917 mRNA partial cds	other
25948	>10	AA234365	Human sapiens survival of motor neuron protein interacting protein 1 (SIP1) mRNA complete cds	?
25951	>10	AA234558	EST	?

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11581	>10	AA236533	E-v-1	other
26059	>10	AA236685	ESTs	other
26100	>10	AA242035	Human mRNA for KIAA0391 gene complete cds	other
11603	>10	AA243052	ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]	other
7785	>10	AA243375	EST - AA243375	other
34372	>10	AA251973	ESTs	?
26240	>10	AA252282	Human mRNA for KIAA0152 gene complete cds	TM
34382	>10	AA252512	ESTs	other
34391	>10	AA252703	EST - RC_AA252703	other
26274	>10	AA253011	ESTs	?
34400	>10	AA253400	ESTs	other
26291	>10	AA253422	ESTs	?
26355	>10	AA256379	ESTs	other
11813	>10	AA258150	ESTs	other
34518	>10	AA278721	ESTs	?
26545	>10	AA278979	ESTs	other
26574	>10	AA279504	ESTs	other
34554	>10	AA280016	DNA polymerase gamma	other
34561	>10	AA280290	ESTs	TM
26628	>10	AA280641	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus]	TM
11969	>10	AA280670	ESTs	SS
34575	>10	AA280738	ESTs	TM
26677	>10	AA281636	ESTs	?
26700	>10	AA282197	EST	?
34672	>10	AA284372	ESTs	other
34692	>10	AA285079	ESTs	other
12143	>10	AA290991	ESTs	other
8092	>10	AA316272	ESTs	TM
34904	>10	AA321746	EST	other
8111	>10	AA323787	ESTs	other
8125	>10	AA330771	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	TM
26916	>10	AA331393	ESTs	other
26926	>10	AA342402	ESTs	other
26935	>10	AA347193	ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans]	TM
35038	>10	AA350541	ESTs Moderately similar to URACIL-DNA GLYCOSYLASE 1 PRECURSOR [H. sapiens]	TM
35049	>10	AA350857	ESTs	other
35106	>10	AA371561	EST Weakly similar to putative p150 [H. sapiens]	?
35197	>10	AA398120	ESTs	other
35277	>10	AA398538	ESTs	other
35309	>10	AA399060	EST	other
35322	>10	AA398710	H. sapiens RNA for CLCN3	TM
27037	>10	AA400198	ESTs	TM
35495	>10	AA400527	ESTs	?
27048	>10	AA400670	Homo sapiens mRNA for KIAA0582 protein partial cds	other
35500	>10	AA400715	ESTs	other
12480	>10	AA403116	Homo sapiens U-snRNP-associated cyclophilin (USA-Cyp) mRNA complete cds	other
35693	>10	AA405485	ESTs Weakly similar to similar to I complex testis-specific protein [C. elegans]	other
35697	>10	AA405512	ESTs	other
35766	>10	AA400169	Homo sapiens KIAA0431 mRNA partial cds	other
35769	>10	AA406206	ESTs	other
35798	>10	AA410231	ESTs	other

FIGURE 8 (cont.)
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35801	>10	AA410291	ESTs	other
35803	>10	AA410295	ESTs	other
35822	>10	AA411144	ESTs	TM
35874	>10	AA412024	EST	?
35958	>10	AA412550	ESTs	other
36052	>10	AA417027	EST	TM
36258	>10	AA423962	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	other
36288	>10	AA424502	ESTs	other
36307	>10	AA424803	EST	?
36371	>10	AA426017	ESTs	TM
36395	>10	AA426353	ESTs	other
36405	>10	AA426408	Homo sapiens mRNA for KIAA0530 protein partial cds	other
36506	>10	AA429610	ESTs	other
36571	>10	AA430726	EST - RC_AA430726	SS,
36695	>10	AA433910	ESTs	other
36739	>10	AA435610	EST - RC_AA435610	?
36753	>10	AA435686	ESTs	other
36845	>10	AA436198	ESTs	?
13136	>10	AA436590	ESTs	SS, TM
13143	>10	AA436619	ESTs	SS,
36958	>10	AA442060	ESTs	other
36982	>10	AA442082	ESTs	?
36981	>10	AA442845	EST	?
13237	>10	AA443971	ESTs Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	?
13242	>10	AA445894	ESTs	other
37057	>10	AA446131	ESTs	other
37068	>10	AA446312	ESTs Weakly similar to !!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]	other
37074	>10	AA446344	ESTs	SS,
37084	>10	AA446486	Homo sapiens Ran binding protein 2 (RanBP2alpha) mRNA partial cds	?
37135	>10	AA447540	EST	?
37159	>10	AA447714	EST - RC_AA447714	other
37168	>10	AA447772	ESTs	?
37246	>10	AA449311	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds	other
37310	>10	AA451707	ESTs	other
37453	>10	AA454610	ESTs	?
37456	>10	AA454832	ESTs	TM
27767	>10	AA454660	ESTs	?
37492	>10	AA455248	EST - RC_AA455248	other
37546	>10	AA456641	ESTs	TM
37601	>10	AA456864	ESTs	other
37611	>10	AA456996	Human signaling lymphocytic activation molecule (SLAM) mRNA complete cds	SS, TM
37615	>10	AA459101	Human serine/threonine kinase mRNA partial cds	other
37653	>10	AA460017	ESTs	other
37677	>10	AA460530	Homo sapiens orphan G protein-coupled receptor HC38 mRNA complete cds	other
37777	>10	AA464860	Homo sapiens Jsk2 kinase mRNA complete cds	other
6548	>10	AA465016	Homo sapiens serine protease-like protease (nest) mRNA complete cds	?
37816	>10	AA469854	EST	?
37829	>10	AA470084	ESTs	other
28015	>10	AA477421	ESTs	other
37978	>10	AA478294	EST - RC_AA478294	other
37978	>10	AA478295	ESTs Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]	other

FIGURE 8 (cont.)

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37963	>10	AA479348	H sapiens mRNA for SYT	other
14094	>10	AA485223	ESTs	TM
38121	>10	AA485724	EST - RC_AA485724	other
28122	>10	AA485928	ESTs Weakly similar to LOK (M.musculus)	other
38167	>10	AA487207	EST - RC_AA487207	other
38172	>10	AA487424	EST - RC_AA487424	other
38178	>10	AA487492	Homo sapiens clone 23592 mRNA sequence	other
38182	>10	AA487501	ESTs	other
38184	>10	AA487669	ESTs	other
28141	>10	AA488432	ESTs	?
38211	>10	AA489687	ESTs	other
38235	>10	AA489030	ESTs	other
38260	>10	AA489791	EST - RC_AA489791	other
38318	>10	AA490500	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds	other
38330	>10	AA490832	ESTs	other
38456	>10	AA504343	ESTs	SS,
38460	>10	AA504462	ESTs	other
38553	>10	AA521471	ESTs	other
38560	>10	AA593545	ESTs	?
38590	>10	AA598548	Human mRNA for transcriptional activator hSNF2b complete cds	other
38601	>10	AA598738	ESTs	?
28323	>10	AA599639	ESTs	other
38828	>10	AA509177	ESTs	TM
38838	>10	AA509215	EST - RC_AA509215	?
38867	>10	AA509318	Human cbl-b mRNA complete cds	TM
38871	>10	AA509333	EST	?
38970	>10	AA509749	ESTs	other
38994	>10	AA509839	ESTs Moderately similar to "H1 ALU SUBFAMILY J WARNING ENTRY "H1 [H.sapiens]	?
39045	>10	AA510077	ESTs	other
39062	>10	AA520333	EST	?
39080	>10	AA520552	EST - RC_AA520552_r	?
39110	>10	AA520709	ESTs Weakly similar to HYPOTHETICAL 80.6 KD PROTEIN TGS10.7 IN CHROMOSOME II [C.elegans]	other
39176	>10	AA521091	ESTs	other
39218	>10	AA521330	ESTs	other
39221	>10	AA521345	Homo sapiens protein phosphatase with EF-hands-1 (PPEF-1) mRNA complete cds	other
39232	>10	AA521409	ESTs	other
21	>10	AB000905	H sapiens histone H4 gene	?
8963	>10	AFFX-HUMTFRRM115 D7	AFFX-HUMTFRRM11507_M	?
33890	>10	AFFX-HUMTFRRM115 C7	AFFX-HUMTFRRM11507_5	?
39302	>10	C14944	ESTs	other
39329	>10	C20797	EST	?
28644	>10	D12153	ESTs	other
218	>10	D13540	PROTEIN-TYROSINE PHOSPHATASE 2C	other
236	>10	D13645	Human mRNA for KIAA0202 gene complete cds	other
9127	>10	D30037	PHOSPHATIDYLINOSITOL	other
459	>10	D38263	Human mRNA for cacthrin-like protein complete cds	TM
33405	>10	D50975	ESTs	other
39433	>10	D52037	Human thymidine kinase 2 (TK2) mRNA complete cds	other
39438	>10	D52692	Human Ca2+-dependent activator protein for secretion mRNA complete cds	TM
14708	>10	D59388	EST	?

FIGURE 8 (cont.)

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39488	>10	D60631	ESTs	other
39504	>10	D60632	ESTs	other
765	>10	D60696	Prostaglandin E receptor 3 (subtype EP3) (alternative products)	?
787	>10	D60699	Human mRNA for KIAA0215 gene complete cds	other
789	>10	D60871	Human mRNA for KIAA0217 gene partial cds	other
39529	>10	F02202	ESTs	?
39535	>10	F02450	ESTs Moderately similar to unknown protein [H.sapiens]	TM
18676	>10	F04022	ESTs	other
18718	>10	F04915	ESTs	other
18762	>10	F09458	ESTs	other
18782	>10	F09739	ESTs	other
29080	>10	F13655	ESTs Moderately similar to H11 ALU SUBFAMILY SB1 WARNING ENTRY H11 [H.sapiens]	other
19001	>10	H02890	ESTs	other
19164	>10	H10285	EST	?
39725	>10	H11323	ESTs	other
19203	>10	H11593	ESTs	other
19328	>10	H17806	ESTs	other
19387	>10	H20128	ESTs	?
39787	>10	H20131	ESTs	SS
19389	>10	H20165	EST	?
39832	>10	H26279	EST - RC_H26279	other
19591	>10	H40688	ESTs	other
29229	>10	H48459	Human mRNA for KIAA0186 gene complete cds	other
19727	>10	H52702	ESTs	?
19787	>10	H56679	ESTs	other
39995	>10	H62474	EST	SS, TM
29331	>10	H68116	ESTs	TM
29344	>10	H68839	EST	?
40064	>10	H72283	Human mRNA for KIAA0265 gene partial cds	other
40083	>10	H73456	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3	other
19949	>10	H78263	ESTs	TM
40204	>10	H88296	EST - RC_H88296	other
29523	>10	H88353	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]	?
29551	>10	H90134	ESTs	?
29645	>10	H95840	ESTs	?
20057	>10	H98079	ESTs	other
976	>10	HG2036-HT2090	EST - HG2036-HT2090	?
1158	>10	HG3344-HT3521	EST - HG3344-HT3521	?
1210	>10	HG37-HT37	EST - HG37-HT37	?
1346	>10	HG4716-HT5158	EST - HG4716-HT5158	?
1349	>10	HG4747-HT5195	EST - HG4747-HT5195	?
1445	>10	J03027	MHC class I protein HLA-G	?
1570	>10	K01383	EST - K01383	?
1684	>10	L07541	Replication factor C (activator 1) 3 (38kD)	other
1852	>10	L17328	Human FEZ2 mRNA partial cds	TM
1856	>10	L18920	MELANOMA-ASSOCIATED ANTIGEN 2	?
1863	>10	L19161	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	other
2070	>10	L37378	Homo sapiens guanylyl cyclase (RcGC-2) mRNA complete cds	SS, TM
2123	>10	L40396	Homo sapiens (clone 422171) mRNA fragment	other
2144	>10	L41349	Phosphopase C beta 4	SS
9723	>10	L44542	ESTs	other
2188	>10	L47276	EST - L47276	other

FIGURE 8 (cont.)

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2343	>10	M15353	Eukaryotic translation initiation factor 4E	other
2627	>10	M29010	Glycophorin E	TM
2857	>10	M58597	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)	TM
3021	>10	M68941	Protein tyrosine phosphatase non-receptor type 4	other
3183	>10	M84424	Cathepsin E	?
3195	>10	M85917	Oxysterol binding protein	other
20088	>10	N20054	ESTs Weakly similar to putative p150 [H.sapiens]	?
29795	>10	N20641	ESTs Highly similar to HYPOTHETICAL MYELOID CELL LINE PROTEIN 3 [Homo sapiens]	other
40427	>10	N21147	ESTs	other
40444	>10	N22140	ESTs Highly similar to TUBULIN GAMMA CHAIN [Euplates octocarinatus]	other
22893	>10	N23003	ESTs	TM
40498	>10	N25086	Homo sapiens citrate synthase mRNA complete cds	SS.
40559	>10	N33024	ESTs	SS.
30190	>10	N33264	EST	?
30207	>10	N33920	H.sapiens mRNA for drubiquitin	other
20304	>10	N34686	Homo sapiens clone 23915 mRNA sequence	?
20307	>10	N34830	ESTs	other
30265	>10	N35115	ESTs	other
40594	>10	N35388	ESTs	other
40604	>10	N38893	Homo sapiens KIAA0428 mRNA complete cds	other
40631	>10	N45124	ESTs	other
40660	>10	N49104	NUCLEAR FACTOR RIP140	other
30810	>10	N50138	EST	?
30617	>10	N50646	ESTs	other
30631	>10	N50807	EST	?
30790	>10	N52935	EST	?
20564	>10	N55443	ESTs	TM
40760	>10	N57827	ESTs Weakly similar to ELL [M.musculus]	other
30838	>10	N58561	Cathepsin B	other
20614	>10	N59230	ESTs	SS.
20657	>10	N62889	ESTs	other
31136	>10	N63512	ESTs Weakly similar to M01F1.4 [C.elegans]	TM
40827	>10	N64051	Homo sapiens Werner syndrome gene complete cds	other
31310	>10	N66831	EST	?
40876	>10	N67607	Human Rho-associated coiled-coil containing protein kinase p16ORCK mRNA complete cds	other
20791	>10	N68057	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds	?
40905	>10	N68738	ESTs	other
40911	>10	N69114	H.sapiens mRNA for orphan nuclear hormone receptor	other
40913	>10	N69218	ESTs	other
31484	>10	N69466	ESTs	other
31619	>10	N73449	ESTs	other
41005	>10	N78516	ESTs	TM
31818	>10	N89774	Homo sapiens mRNA for KIAA292 gene partial cds	other
31872	>10	N91109	EST	other
41040	>10	N91946	ESTs	other
31944	>10	N93193	ESTs	other
41065	>10	N93618	ESTs	other
32034	>10	N95926	ESTs Moderately similar to DMR-N9 PROTEIN [H.sapiens]	other
41107	>10	R01634	ESTs	other
41163	>10	R08176	ESTs	other
21238	>10	R08564	Plasminogen-like protein	other

FIGURE 8 (cont.)

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21240	>10	R08513	ESTs	other
21412	>10	R20670	ESTs	other
21519	>10	R27975	EST - RC_R27975	other
41381	>10	R42278	H sapiens mRNA for TRE5	?
32189	>10	R43183	ESTs	TM
32195	>10	R43471	ESTs Weakly similar to ORF YOR258w [S cerevisiae]	other
21902	>10	R43822	EST	?
21946	>10	R44707	ESTs	TM
22072	>10	R49406	ESTs	?
32240	>10	R50976	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor	other
32258	>10	R55823	ESTs	other
22258	>10	R56432	ESTs	other
22282	>10	R59187	ESTs	other
32277	>10	R61493	Human mRNA for rod photoreceptor protein complete cds	other
22372	>10	R62831	EST	?
22400	>10	R64109	ESTs	other
41583	>10	R64129	ESTs	other
10233	>10	R71427	ESTs Highly similar to PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN CYTOPLASMIC [Saccharomyces cerevisiae]	other
41854	>10	R76437	THROMBOXANE-A SYNTHASE	TM
22557	>10	R76722	ESTs	other
22576	>10	R79111	ESTs	other
22593	>10	R79777	EST	?
41678	>10	R80675	EST	?
41719	>10	R89280	EST - RC_R89280	other
22783	>10	R96208	ESTs	other
41752	>10	R97063	ESTs	other
3375	>10	S50223	HKR-T1	other
3406	>10	S68896	SQUAMOUS CELL CARCINOMA ANTIGEN 1	other
3522	>10	S80267	Spleen tyrosine kinase	other
41793	>10	T03887	ESTs	?
23198	>10	T40530	ESTs Weakly similar to B0035.14 [C elegans]	other
23360	>10	T58531	ESTs	other
32635	>10	T61116	ESTs	other
42177	>10	T79786	ESTs	?
23623	>10	T84047	ESTs	?
23662	>10	T86674	ESTs	other
42242	>10	T89579	Human sapiens E2F-related transcription factor (DP-1) mRNA complete cds	other
23759	>10	T90313	ESTs	other
23832	>10	T92018	ESTs	other
32740	>10	T92950	ESTs	other
42790	>10	T95105	ESTs	?
3598	>10	U01157	Glucagon-like peptide-1 receptor	SS, TM
3659	>10	U04313	Protease inhibitor 5 (maspin)	other
3799	>10	U10690	Human MAGE-5a antigen (MAGE5a) gene complete cds	?
3870	>10	U14518	Centromere protein A (17kD)	other
3913	>10	U16261	Human MDA-7 (mda-7) mRNA complete cds	SS,
4029	>10	U21090	Human DNA polymerase delta small subunit mRNA complete cds	other
4157	>10	U28811	Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA complete cds	other
4178	>10	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM
15006	>10	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM

FIGURE 8 (cont.)

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4193	>10	U31116	Human beta-keroglycan A3b mRNA complete cds	TM
4306	>10	U36798	Homo sapiens platelet cGMPDE mRNA complete cds	TM
4362	>10	U35817	Bloom syndrome	other
4386	>10	U40622	DNA repair protein XRCC4	other
4388	>10	U40714	Human tyrosyl-tRNA synthetase mRNA complete cds	other
4455	>10	U43944	MALATE OXIDOREDUCTASE	other
4477	>10	U45880	Human IAP-like protein ILP mRNA complete cds	other
4500	>10	U55766	Human Rev interacting protein Rip-1 mRNA complete cds	TM
4702	>10	U57341	EST - U57341	other
4713	>10	U57721	Human L-lysine hydrolase mRNA complete cds	other
4787	>10	U61145	Human enhancer of zeste homolog 2 (EZH2) mRNA complete cds	other
4862	>10	U65437	Human homodomain-containing protein (HAMP) mRNA complete cds	?
4845	>10	U69108	Homo sapiens mRNA for TRAF5 complete cds	other
4976	>10	U71088	Human MEK5 mRNA complete cds	other
4994	>10	U72514	Human C2I mRNA complete cds	other
5002	>10	U72761	Human karyopherin beta 3 mRNA complete cds	other
5021	>10	U73524	Human oxidative ATPGTP-binding protein (HEAB) mRNA complete cds	TM
5149	>10	U79716	Human rotein (RELN) mRNA complete cds	SS
5214	>10	U83303	H. sapiens mRNA for granulocyte chemotactic protein	?
5243	>10	U85946	Human brain secretory protein hSec10p (HSEC10) mRNA complete cds	other
52789	>10	W02779	ESTs Moderately similar to kinesin-73 (D.melanogaster)	other
42354	>10	W19346	ESTs	other
42390	>10	W40150	Homo sapiens chromosome-associated polypeptide (HICAP) mRNA complete cds	other
33006	>10	W46286	ESTs Weakly similar to ZK1058.5 (C.elegans)	TM
33070	>10	W46891	ESTs Weakly similar to polypeptide N-acetylglucosaminyltransferase (H.sapiens)	other
33109	>10	W59961	Human mRNA for KIAA0369 gene complete cds	other
24197	>10	W67277	ESTs	other
24215	>10	W69425	ESTs	other
33301	>10	W73883	ESTs	other
33343	>10	W79834	ESTs Weakly similar to thotekin (M.musculus)	other
33377	>10	W81219	ESTs Weakly similar to F46B5.7 (C.elegans)	other
47602	>10	W86423	ESTs	TM
33556	>10	W90705	Murine leukemia virus (bmi-1) oncogene homolog	other
33616	>10	W93726	Protease inhibitor 5 (maspin)	other
33666	>10	W93876	ESTs	TM
5510	>10	X05360	Cell division cycle 2 G1 to S and G2 to M	?
5558	>10	X07878	Wingless-type MMTV integration site 2 human homolog	SS
5603	>10	X14253	Tarascarcinoma-derived growth factor 1	TM
5619	>10	X14850	HISTONE H2A.X	SS
5623	>10	X14979	T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR	?
5692	>10	X17644	G1 to S phase transition 1	other
5789	>10	X54925	Matric metalloproteinase 1 (interstitial collagenase)	other
5799	>10	X55330	Aspartylglucosaminidase	SS
5802	>10	X55544	CYCLOC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-1	?
5857	>10	X58377	Human mRNA for edpogenesis inhibitory factor	other
5960	>10	X63575	ATPase Ca++ transporting plasma membrane 2 (NOTE redefinition of symbol)	TM
5963	>10	X63629	Cadherin 3 (P-cadherin)	SS, TM
5986	>10	X04810	Protein convertase subtilisin/kexin type 1	?
6041	>10	X67152	MITOTIC KINESIN-LIKE PROTEIN-1	other
6095	>10	X69962	Fragile X mental retardation 1	other

FIGURE 8 (cont.)

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6106	>10	X70683	SRY (sex determining region Y)-box 4	TM
6155	>10	X74331	DNA primase polypeptide 2A (58kD)	other
6167	>10	X74987	Recombinase L (75'-oligonucleotide synthetase-dependent) rNucR	other
6182	>10	X76029	NEUROMEDIN U-25 PRECURSOR	TM
6316	>10	X81889	H. sapiens mRNA for p0071 protein	other
6382	>10	X85133	H. sapiens RBQ-1 mRNA	other
6384	>10	X85137	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds	other
6438	>10	X89388	URACIL-DNA GLYCOSYLASE 1 PRECURSOR	?
6449	>10	X89886	H. sapiens mRNA for NBK apoptotic inducer protein	TM
6478	>10	X91648	H. sapiens mRNA for put alpha extended 3'untranslated region	SS, TM
6479	>10	X91653	EST - X91653	?
6494	>10	X92689	H. sapiens mRNA for UDP-GalNAc:polypeptide N-acetylglucosaminyl transferase	TM
6713	>10	Y08564	EST - Y08564	?
6790	>10	Y12394	Human sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds	other
24915	>10	YEL003w	EST - YEL003w	?
42773	>10	YEL019cMM521	EST - YEL019cMM521	?
24545	>10	Z38462	ESTs	other
33713	>10	Z39427	ESTs	other
33791	>10	Z40883	ESTs	other
42766	>10	Z99394	ESTs Moderately similar to III ALU SUBFAMILY SP WARNING ENTRY III [H. sapiens]	other
21558	>10	R33112	Human AF-6 mRNA complete cds	other
25718	>10	AA282576	ESTs	?
40113	9 9955090946	H78003	ESTs	?
13801	9 8879448276	AA032805	ESTs Weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 [C. elegans]	other
37491	9 9513600842	AA55239	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN OPY-27 [Caenorhabditis elegans]	other
23800	9 8272347693	T95789	ESTs	other
254	9 9188395324	D14657	Human mRNA for KIAA0101 gene complete cds	other
6885	9 8970927914	Z28331	Ubiquitin-conjugating enzyme E2H (homologous to yeast UBC8)	other
29683	9 8850706398	H97819	ESTs	SS,
26482	9 8765189024	AA262491	ESTs	other
23123	9 8699902095	T25306	EST	?
26525	9 8160399123	AA278352	ESTs	other
13110	9 7643356605	AA435840	Human sapiens mRNA for high mobility group protein HMGB2a	other
34863	9 7087597628	AA299784	EST	other
39432	9 7034550063	D51691	Phosphoribosylglycnamide formyltransferase phosphoribosylglycnamide synthetase phosphoribosylhomodazole synthetase	?
31312	9 6513326388	N66845	ESTs Weakly similar to III ALU CLASS B WARNING ENTRY III [H. sapiens]	?
21112	9 6358446349	R01179	ESTs	?
31572	9 6254820095	N71294	ESTs	other
17903	9 6221229759	AA160259	EST	?
20747	9 6094813734	N66842	ESTs	other
4676	9 589223908	U55206	Human sapiens human gamma-glutamyl hydrolase (hGH) mRNA complete cds	TM
34363	9 5627081023	AA251587	Human sapiens mRNA for KIAA0530 protein partial cds	other
28094	9 540768688	AA620636	ESTs	other
3888	9 5372000133	U15128	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds	?
39386	9 506250529	D12184	ESTs	TM
7674	9 4458059039	AA203742	ESTs	other
4192	9 4329744134	U31099	Human DP prostanoicd receptor (PTGDR) mRNA partial cds	TM
4507	9 422874945	U47050	Human putative calcium influx channel (hcap3) mRNA complete cds	TM

FIGURE 8 (cont.)

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35606	9 412026255	AA02227	ESTs Moderately similar to N-economodulin (R norvegicus)	other
4970	9 3648551013	U70862	Human nuclear factor I-B2 (NFIB2) mRNA complete cds	?
19829	9 3432151573	H58813	EST	?
14837	9 2878504141	T40145	ESTs	TM
17336	9 2822140675	AA099585	ESTs	other
40541	9 2532636505	N30160	ESTs	other
29496	9 2487643613	H85434	EST	?
29943	9 1767074262	N24766	ESTs Moderately similar to (III) ALU SUBFAMILY J WARNING ENTRY !!! (H sapiens)	TM
17997	9 1629681314	AA169633	EST	other
21320	9 1243463316	R11673	ESTs	other
13853	9 1178796537	AA476917	ESTs Weakly similar to No definition line found (C.elegans)	other
30539	9 0886887776	N49072	ESTs	other
32778	9 0877919549	WQ2063	EST	?
26380	9 0809559378	AA257012	EST	?
15888	9 059583607	X95832	Human Abi interactor 2 (Abi-2) mRNA complete cds	other
40812	9 0012874244	N63419	ESTs	other
903	8 9640387908	D90070	ATL-derived PMA-responsive (APR) peptide	other
22674	8 9515777733	R87160	ESTs	TM
40807	8 9510132281	N62995	TRANSCRIPTION INITIATION FACTOR IF BETA SUBUNIT	other
15244	8 9185644974	WQ0904	ESTs	TM
32296	8 8858778567	R87075	Zinc finger protein X-linked	other
18269	8 8575656769	AA209467	ESTs	other
19662	8 8507620284	H47391	ESTs	other
41807	8 833925517	R87868	CLEAVAGE SIGNAL-1 PROTEIN	other
2548	8 8298864659	M25897	Platelet factor 4	TM
7736	8 8279341243	AA232121	Human tyrosyl-tRNA synthetase mRNA complete cds	other
34490	8 7844537272	AA262354	ESTs	other
38658	8 7668313482	AA599477	ESTs	other
7528	8 765157554	AA149543	ESTs	other
39939	8 7555031142	H53454	EST - RC_H53454	other
25111	8 7232892309	AA020787	ESTs	other
21655	8 716167279	R38239	EST	?
39663	8 665982652	H04756	ESTs Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (Bos taurus)	other
1042	8 652112324	HG2510-HT2608	EST - HG2510-HT2608	?
32330	8 6361115426	R77776	ESTs	other
25382	8 6239450487	AA059007	ESTs	other
27074	8 5900813076	AA401475	ESTs Weakly similar to C36B1.3 (C.elegans)	SS
3955	8 5298909183	U18259	MHC class II transactivator	other
4959	8 52646027	U70322	Human transportin (TRN) mRNA complete cds	other
2315	8 5259185808	M14123	EST - M14123_xp11	?
37253	8 4896914632	AA449357	ESTs	other
39624	8 471316877	F10836	ESTs	?
23213	8 4569920887	T40891	ESTs	?
2708	8 455596435	M54995	Connective tissue activation peptide III	TM
41154	8 4413390141	R07499	ESTs	?
32479	8 4093689549	T18282	WEE1-LIKE PROTEIN KINASE	other
41251	8 3587565415	R28279	Human clone 23548 mRNA sequence	other
19081	8 3583603183	H06701	ESTs Weakly similar to RHOMBOTIN-1 (H sapiens)	other
21098	8 3105877559	R00545	ESTs	other
14723	8 3061679053	D58854	ESTs	other
37154	8 2994822341	AA447666	Human CENP-F kinetochore protein mRNA complete cds	other

FIGURE 8 (cont.)

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6066	8 2835566361	AA313367	ESTs Highly similar to HYPOTHETICAL 847 cD PROTEIN ZK1098.1 IN CHROMOSOME III [Caenorhabditis elegans]	other
7485	8 281678048	AA129547	ESTs	other
16501	8 251796834	AA026968	ESTs	other
34527	8 2418163754	AA279091	ESTs	other
6700	8 1948675662	Y07867	HeLa cells mRNA for Pen isolate 1	other
2852	8 1928816537	M58480	Human 75-kD autoantigen (PK-Scl) mRNA complete cds	other
11188	8 1862492468	AA172372	ESTs	TM
42283	8 183311064	T95333	ESTs Weakly similar to coded for by C. elegans cDNA y110g8.3 [C. elegans]	TM
5443	8 1783317544	X02530	Interferon (gamma)-induced cell line protein 1C from	SS.
40837	8 1534810594	N70607	ESTs	TM
23371	8 1499496068	T59505	EST - RC_T59505	?
26272	8 1339974519	AA252981	ESTs Weakly similar to K07C11.10 gene product [C. elegans]	other
17306	8 1332403782	AA086201	ESTs	other
18497	8 1182326373	AA233795	ESTs	other
235	8 0944363901	D13644	Human mRNA for KIAAC19 gene complete cds	other
24525	8 0860187097	Z38347	ESTs	TM
7828	8 0760028554	AA240884	EST - AA240884	TM
32142	8 0730258775	R38715	Human sapiens clone 24540 mRNA sequence	other
39067	8 0557768803	AA620405	ESTs	other
6235	8 0448957236	X78416	Casein alpha S1	TM
28617	8 0017588725	H88261	ESTs	other
28570	7 9852456973	C21104	Human sapiens STAT-induced STAT inhibitor-2 mRNA complete cds	other
39344	7 9162587762	C21034	ESTs Moderately similar to mutation factor siF-2B gamma subunit [R. norvegicus]	other
18951	7 9002189759	H00580	ESTs	other
18953	7 8709160227	M00615	ESTs	other
18376	7 8564099916	AA225925	ESTs	other
19830	7 847878447	H58911	ESTs	other
36023	7 840835628	AA418831	ESTs	other
13347	7 8344414518	AA449238	ESTs	other
36614	7 8284591351	AA431466	ESTs	other
2192	7 8254072032	L48211	Human Sapiens angiotensin II receptor gene complete cds	?
33016	7 8006574068	V46577	Human sapiens mRNA for ESM-1 protein	other
17215	7 7941954038	AA083044	ESTs	other
34894	7 7658738105	AA311881	EST	?
40814	7 7595001222	N39257	ESTs	other
36295	7 6834749899	AA424534	ESTs	other
19564	7 6744302788	H38833	ESTs	TM
16914	7 6686405336	AA055665	ESTs	SS.
35967	7 6378079107	AA412694	Human splicing factor SRp55-2 (SRp55) mRNA complete cds	other
21872	7 6364823402	R38635	ESTs	other
19918	7 6303275831	H59787	ESTs	?
10511	7 6297744492	AA024482	ESTs Highly similar to KERATIN TYPE I CYTOSKELETAL 14 [Homo sapiens]	other
17721	7 6057911016	AA136590	ESTs	?
42302	7 6031856097	T96130	EST	SS.
26134	7 6000619583	AA243763	ESTs	other
18766	7 5631799006	F09497	ESTs	other
34482	7 501560494	AA282439	ATL-derived PMA-responsive (APR) peptide	other
270	7 4512152125	D14822	EST - D14822	other
35975	7 4177746966	AA412738	ESTs	other
29842	7 4085806071	N21688	ESTs	?

FIGURE 8 (cont.)

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35389	73913043319	AA398555	ESTs	other
19979	73868157166	H88477	ESTs	other
5793	73865864025	X54942	CDC28 protein kinase 2	other
19978	73309697115	H87770	EST - RC_H87770	other
1280	73691089318	HG4126-HT4396	EST - HG4126-HT4396	?
31571	73676263454	N71250	ESTs	other
23765	73541191734	T90443	ESTs Weakly similar to KIAA0376 [H.sapiens]	?
35123	73397933455	AA380927	EST	?
38252	733411119467	AA455247	ESTs	other
38218	73282021037	AA488861	ESTs	other
29418	72489407005	H77915	EST - RC_H77915	?
4834	71980951054	U63541	Human mRNA expressed in HCHCC livers and Molt-4 proliferating cells partial sequence	other
42504	71813036522	V69803	ESTs	other
5111	7158000189	X71125	H.sapiens mRNA for glutamine cyclotransferase	TM
41773	7154479618	T03024	ESTs Weakly similar to ribosomal protein L7 [H.sapiens]	other
9951	71363626365	N71513	ESTs	other
28109	70941960224	AA485212	ESTs	other
968	70783044658	HG2160-HT2230	EST - HG2160-HT2230	?
29848	70610608511	N22107	ESTs	other
30628	70627950168	N50744	ESTs	other
22567	70225726353	R77771	ESTs	TM
9347	7006323071	H03686	ESTs	TM
11698	70026773299	AA252894	ESTs	other
40584	70010096333	N34870	EST	?
193	69767029188	D10823	PROBABLE G PROTEIN-COUPLED RECEPTOR HW74	TM
18305	69740539051	AA214048	Collagen type IV alpha 4	other
6078	69699682397	X09141	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE	other
26741	6902658703	AA233198	ESTs	other
35069	6892865685	AA358397	EST	?
23504	68977135883	T71042	ESTs	other
299	68824513029	D16815	Human sapiens orphan nuclear hormone receptor BD73 mRNA 3' end	other
40583	68689903023	N34855	ESTs	other
31428	68623762274	N68594	ESTs	other
6169	68606959727	X75091	SET PROTEIN	other
39524	68567355171	F01805	MALATE OXIDOREDUCTASE	other
34578	68430689439	AA280637	ESTs	other
38678	6837527995	AA599920	Small inducible cytokine A5 (RANTES)	other
23936	68251471804	T96930	ESTs	other
9326	68181321394	D89377	Msh (Drosophila) homeo box homolog 2	other
19188	68087351958	H11255	ESTs Highly similar to ACTIN-LIKE PROTEIN (Box taurus)	TM
18185	67882148811	AA194983	Human sapiens mRNA for osteoclastogenesis inhibitory factor (OCIF) complete cds	other
27029	6757529124	AA399630	ESTs Weakly similar to KIAA0371 [H.sapiens]	other
41289	67519531681	R37265	EST	other
34511	67364448758	AA278299	EST - RC_AA278299	other
1566	67056207716	J05614	EST - J05614	?
25675	66932299748	AA129757	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]	other
5814	66584342828	X56088	CYTOCHROME P450 VII	SS
13861	66236291607	AA470145	ESTs	other
29794	66026313352	N20598	ESTs	other
39333	65902382643	C20910	Cyclin B1	other
3770	65835303599	U09609	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p48/p100)	other

FIGURE 8 (cont.)

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31831	5 5829933764	N59894	ESTs	?
33063	5 5806125026	W53000	Homo sapiens clone 24431 mRNA sequence	other
20328	5 5640084836	N35583	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 56]	?
34384	5 5535703492	AA252537	ESTs	other
25599	5 5490481991	AA114091	Human (clone BB1) Br-cadherin mRNA complete cds	other
39749	5 53659363254	H14988	ESTs	other
42596	5 5230567072	W85900	ESTs	?
39008	5 5119482185	F10243	ESTs Weakly similar to III ALU CLASS B WARNING ENTRY !!!! [H.sapiens]	?
14817	5 5103504748	C14983	ESTs	other
27831	5 45870814	AA455044	ESTs	?
34896	5 4496517783	AA312551	EST	?
27360	5 4434305006	AA425358	ESTs	other
20126	5 4326610424	N22015	ESTs	TM
6683	5 4324809977	Y00291	RETINOIC ACID RECEPTOR BETA 2	TM
30692	5 4196036207	N51563	ESTs	other
36472	5 4189542265	AA428633	EST	?
9578	5 3961788753	K07852	Homo sapiens ocaudal-D (BICD) mRNA complete cds	other
39670	5 3818496159	H05626	ESTs	other
22697	5 3652792447	R59218	ESTs	other
37308	5 3647804993	AA451694	EST	TM
16101	5 3517262802	AA002147	EST	?
20629	5 3486854401	N59798	ESTs	other
36100	5 3384146287	AA417740	ESTs	?
15488	5 3252580241	V28097	Homo sapiens clone 23711 unknown mRNA partial cds	other
30867	5 3131273544	AA432136	ESTs	other
30766	5 3115037824	N52627	EST - RC_N52627	?
32882	5 2745311453	W07683	ESTs	TM
18072	5 2675797205	AA180448	EST	?
18231	5 2652604863	AA199747	Human mRNA for KIAA0096 gene partial cds	other
38282	5 2514165678	AA489814	EST	?
28125	5 250317021	AA486073	ESTs	other
37464	5 2484456382	AA454747	ESTs	?
36618	5 1946328223	AA431478	ESTs	other
5082	5 1931116815	U78524	Human Gv binding protein mRNA partial cds	other
1441	5 1777287009	J02963	Integrin alpha 2b (platelet glycoprotein IIb of fibrin complex antigen CD41B)	other
42105	5 14875944	T87710	ESTs	?
6061	5 1394863141	X58314	Glutathione peroxidase 2 gastrointestinal	SS
32570	5 1156026796	T30222	ESTs Weakly similar to tetracycline transporter-like protein [M.musculus]	TM
32504	5 1018612076	T17063	EST	?
23335	5 0977827604	T56804	EST	?
10867	5 0970991076	AA088458	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	other
30883	5 0911993489	N56923	EST	?
14528	5 0859008453	AA620295	ESTs	TM
29454	5 0685955036	H81306	EST	?
6758	5 0539173278	V13153	Homo sapiens mRNA for kynurenine 3-monooxygenase	TM
21248	5 0525426545	R08871	ESTs	?
21940	5 0499984138	R44538	ESTs	?
29006	5 0455247653	F10927	Homo sapiens clone 23636 mRNA sequence	other
18774	5 0446826953	F09609	ESTs	?
30722	5 0172341891	AA435512	ESTs	SS
18062	5 0034342989	AA179845	ESTs Moderately similar to rabkinasin-6 [M.musculus]	other

FIGURE 8 (cont.)

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22689	5.9952817406	T16305	ESTs	other
41745	5.9905623398	R95853	ESTs	?
8787	5.9894877658	AA504307	X-LINKED HELICASE II	other
20530	5.984861785	N55013	ESTs	other
26470	5.9417784101	AA282178	ESTs	other
16574	5.9356497569	AA031926	EST	other
693	5.9169537305	D80007	Human mRNA for KIAA0185 gene partial cds	other
4093	5.914530973	U25182	Human endoxonin enzyme AOE37-2 mRNA complete cds	TM
1182	5.9086264407	HG3546-HT3744	EST - HG3546-HT3744	?
22850	5.8954735623	T10248	ESTs	other
36723	5.891606409	AA435524	EST	?
2114	5.8844498595	L40084	EST - L40384	other
26872	5.868238789	AA291137	ESTs	other
6602	5.8683883018	X98266	EST - X98266_cds2	other
42701	5.8594483433	Z38912	ESTs	other
26573	5.84591116	C21118	ESTs	other
18290	5.8189427695	AA211901	ESTs	other
732	5.8043917841	D83781	Human mRNA for KIAA0197 gene partial cds	other
5330	5.8014145811	U91327	EST - U91327	?
33503	5.7990715189	W88720	EST	?
2353	5.7787505864	M26167	Human platelet factor 4 variation 1 (PF4var1) gene complete cds	?
34705	5.7658906254	AA286907	ESTs Weakly similar to putative p150 [H.sapiens]	other
42663	5.7594091043	W93659	ESTs	other
38180	5.7539310793	AA487495	EST - RC_AA487495	other
4244	5.7476738806	U33286	Human chromosome segregation gene homolog CAS mRNA complete cds	other
32822	5.7418957453	V16834	ESTs	TM
3677	5.7245885557	U18991	Retinal pigment epithelium-specific protein (E51D)	?
24673	5.7202366155	Z38301	ESTs	TM
6328	5.7120261126	Z46629	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversion)	other
35726	5.7030796258	AA508733	ESTs	?
33290	5.6882372058	C14573	Human mRNA for KIAA0029 gene partial cds	other
11405	5.6818873796	AA232231	ESTs	other
22538	5.6782005591	R73567	Homo sapiens matrix-L precursor (ADAM12) mRNA complete cds	TM
40747	5.6605393208	N56672	Homo sapiens clone 22 mRNA alternative splice variant alpha-1 complete cds	TM
31596	5.6554024604	N72094	ESTs	other
6329	5.6415652518	X82279	EST - X82279	?
31578	5.6273323861	N71361	ESTs	other
33207	5.6271818482	W70051	H.sapiens mRNA for M-phase phosphoprotein mop9	other
2545	5.6105880146	M25753	Cyclin B1	other
22580	5.5988402647	R79156	ESTs	other
33592	5.5935314518	W83127	ESTs	other
28843	5.5734698755	D60252	ESTs	other
6160	5.5689050619	X74784	CDC21 HOMOLOG	other
37987	5.561345667	AA479668	ESTs	other
42515	5.5217868811	W72116	Homo sapiens clone 23622 mRNA sequence	other
4732	5.5130666527	U58522	Human huntingtin interacting protein (HIP2) mRNA complete cds	other
3299	5.5099850678	M95623	Hydroxymethylglutamate synthase	?
28320	5.473406981	AA599574	ESTs	?
748	5.471280899	D84454	Human mRNA for UDP-galactose 4-epimerase complete cds	TM
39373	5.4635004954	C21517	ESTs	other
3117	5.4338413537	M81182	Peroxisomal membrane protein 1 (70LD Zellweger syndrome)	other

FIGURE 8 (cont.)

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21257	5 4343612441	R09196	ESTs Moderately similar to M-phase phosphoprotein 11 [H.sapiens]	other
31487	5 4318648859	H69507	ESTs	other
28954	5 4137130511	F03153	ESTs	other
38328	5 328782721	AA602595	ESTs	other
29903	5 3722320822	N23366	EST	?
30525	5 3437432315	N58295	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]	?
19091	5 3344815899	H07864	ESTs	TM
28209	5 3138651018	AA491250	ESTs	other
9470	5 3118897884	H46617	EST - H46617	other
9435	5 3070056656	H30201	EST - H30201	?
28552	5 2954432572	C20914	ESTs	other
27411	5 2940164267	AA428137	ESTs	other
30615	5 2924125284	N50558	ESTs	other
28313	5 2657877167	AA599309	ESTs	TM
39321	5 2649035384	C20632	ESTs	?
29934	5 2531047395	N24194	ESTs	other
1094	5 2496703122	HG2846-HT2983	EST - HG2846-HT2983	?
35578	5 2481126384	F08925	ESTs	TM
11232	5 2466789424	AA186804	ESTs Weakly similar to unknown [S.cerevisiae]	other
2466	5 2426349328	M21539	Human small proline rich protein (spr1) mRNA clone 1292	other
26843	5 2387758661	AA287450	ESTs	?
40331	5 2353385567	H97562	ESTs Weakly similar to SPERMATID-SPECIFIC PROTEIN T2 [Sepia officinalis]	other
6033	5 205798385	AA305116	EST - AA305116	other
29793	5 1955425722	N20593	ESTs Weakly similar to weak similarity to procoagogen alpha chain 1(V) chain [C.elegans]	other
34109	5 1481600107	AA210722	EST	?
26408	5 1432577257	AA258177	ESTs Weakly similar to ROSA26AS [M.musculus]	other
19263	5 1427029807	H15054	ESTs	TM
24596	5 1416089352	Z35810	ESTs	other
28589	5 1365059753	C21245	H.sapiens mRNA for apoptosis specific protein	other
5684	5 1121931412	X17098	Pregnancy-specific beta-1 glycoprotein 6	other
30710	5 1078347344	N51781	EST	?
35785	5 0973514948	AA406167	EST	?
26360	5 0883127861	AA258460	ESTs	?
2351	5 0649012092	M15796	Proliferating cell nuclear antigen	?
30262	5 0636877534	N35065	Homo sapiens clone 24739 mRNA sequence	other
41782	5 0737512465	T03886	ESTs	?
36710	5 0703839864	AA434411	ESTs	other
39090	5 0546585407	AA520628	ESTs	TM
42185	5 0539926381	T78951	ESTs	?
18745	5 0460321557	F09134	ESTs	other
35746	5 0386841896	AA406063	ESTs	other
35356	5 0354809581	AA399053	EST	?
36769	5 0312706878	AA435750	EST	?
36900	5 0278911548	AA436866	H.sapiens mRNA for M-phase phosphoprotein mpp9	other
27595	5 0244757301	AA443328	ESTs	TM
16290	5 0056611904	AA016145	ESTs	?
27117	5 0016146599	AA405099	ESTs Weakly similar to MCESIN/EZRIN/RADKIN HOMOLOG [D.melanogaster]	other
4304	4 9951654397	U36754	Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit	other
33458	4 9907402071	V06635	Homo sapiens mRNA for KIAA0536 protein complete cds	other
26693	4 9800090876	AA282120	EST	?
12669	4 9758138651	AA417030	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	other

FIGURE 8 (cont.)
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29701	4 9706520307	H97970	EST	?
20483	4 9557253836	H52168	ESTs	TM
8720	4 9439110002	AA481218	EST - AA481218	other
34828	4 9431269475	AA292436	Homo sapiens semaphorin F homolog mRNA complete cds	SS, TM
14965	4 941821032	U15128	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds	?
16115	4 9377553532	AA004420	ESTs	?
42506	4 9348587118	V70074	EST	other
34781	4 9316837445	AA287833	ESTs	other
11870	4 9281056201	AA262587	ESTs	TM
23211	4 9256391854	T40880	ESTs	other
40611	4 9160502275	N39138	Homo sapiens mRNA for KIAA0504 protein partial cds	other
42611	4 9128605354	V87006	Homo sapiens putative RNA binding protein KOC (koc) mRNA complete cds	other
39652	4 9045174505	H03099	ESTs	other
17581	4 889874761	AA126395	EST	?
37239	4 8704375389	AA449121	ESTs	?
18712	4 8703618781	F04077	ESTs	other
30709	4 8611171953	N51752	ESTs Weakly similar to synapse-associated protein 99/47-1 [D. melanogaster]	other
34179	4 8503613948	AA227903	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]	?
21433	4 825670988	R22183	EST	?
39731	4 8186142741	H11760	ESTs	other
31295	4 8116814607	N66553	ESTs	other
24647	4 8041830555	Z39108	EST	?
31292	4 8008871817	N68815	ESTs	other
1285	4 7897542383	HQ4157-HT4427	EST - HG4157-HT4427	?
11106	4 7932425858	HG2981-HT3127	EST - HG2981-HT3127	?
18212	4 7812202505	AA190506	ESTs	other
34367	4 782207045	AA251758	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds	other
34802	4 7797760205	AA291468	ESTs	TM
34762	4 7775301548	AA287834	ESTs	other
11595	4 7696612848	AA242819	ESTs	other
8295	4 7639839111	AA405082	ESTs	?
17622	4 758635576	AA131584	ESTs Weakly similar to SOP1 PROTEIN [Saccharomyces cerevisiae]	other
35781	4 7572463523	AA406335	ESTs	other
34754	4 7483874972	AA287642	Human mRNA for KIAA0078 gene complete cds	other
23237	4 7444854356	T47291	EST	?
37667	4 7280445357	AA460318	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L26 [Rattus norvegicus]	other
11588	4 7257189975	AA238786	ESTs	other
38622	4 7190695733	AA598967	ESTs	?
5137	4 7057359474	U79206	Dihydrokocamide S-acyltransferase (E2 component of pyruvate dehydrogenase complex)	other
25038	4 7002244720	AA010065	CDC28 protein kinase 2	other
18288	4 7000147312	H16567	ESTs	other
32503	4 6979488292	T17045	Collagen type I alpha-2	other
3278	4 6953739298	M94055	SODIUM CHANNEL PROTEIN BRAIN II ALPHA SUBUNIT	TM
9696	4 6942061018	L38961	Integral transmembrane protein I	TM
35400	4 6901390898	AA395991	Homo sapiens putative DNA methyltransferase (DNMT2) mRNA complete cds	other
35248	4 6862691303	AA398367	EST Weakly similar to HSP60 protein [M. musculus]	?
36387	4 6827499271	AA426270	ESTs	other
21509	4 6730072542	R27314	ESTs	other
31381	4 6729672124	N67889	ESTs	other
26723	4 6727894925	AA282781	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP28 [Saccharomyces cerevisiae]	other

FIGURE 8 (cont.)

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36326	4 6703621086	AA425151	human GAP SH3 binding protein mRNA complete cds	other
17409	4 6688418667	AA113136	EST - RC_AA113136	other
4908	4 6552339935	U67156	Human mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA complete cds	other
30594	4 6496236326	N49267	ESTs	other
36286	4 64639735	AA488847	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycticebus coucang]	?
13073	4 6426509459	AA433950	ESTs	other
40435	4 6240181066	N21614	Homo sapiens basic-leucine zipper transcription factor MafG (MAFG) mRNA complete cds	other
14474	4 6228694378	AA609427	ESTs Moderately similar to III ALU SUBFAMILY 5C WARNING ENTRY III [H.sapiens]	other
38213	4 615309907	AA488847	ESTs Weakly similar to putative p150 [H.sapiens]	?
5312	4 606644180	U90716	Human cell surface protein NCAR mRNA complete cds	SS, TM
24225	4 6041550359	W70326	ESTs	?
35988	4 5068982366	AA401750	EST	?
26739	4 50663195051	H99626	EST	?
7203	4 5782992577	AA053096	EST - AA053096	other
2157	4 5772055869	L41839	Homo sapiens protein-tyrosine kinase EPHB2 (EPHB2) mRNA complete cds	SS, TM
32086	4 5661024279	R11510	ESTs	?
8085	4 5648114738	AA314776	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]	SS
224	4 5622018989	D13633	Human mRNA for KIAA0008 gene complete cds	other
34006	4 5609980241	AA188761	DNA polymerase gamma	other
33656	4 5557384389	W95477	ESTs	other
34005	4 5537335124	AA195517	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	TM
6028	4 5357822087	X66503	Adenylosuccinate synthase	other
4166	4 5032930671	U29483	Cytochrome B561	?
40262	4 5024727522	H93567	ESTs	TM
22687	4 5018672549	R88209	ESTs	TM
41069	4 4977510482	N95989	H.sapiens mRNA for NF-AT protein	SS
8264	4 4793100575	AA401334	ESTs	other
27588	4 472017297	AA443187	ESTs	other
35882	4 4717575552	AA412047	ESTs	?
34478	4 465518181	AA252080	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM
15921	4 4548516436	Y12065	Homo sapiens mRNA for nuclear protein hnRnp56	?
11279	4 4380038671	AA195399	ESTs	other
39222	4 4367650786	AA821348	ESTs Highly similar to DOULCHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae]	other
34428	4 4364736766	AA256526	ESTs	other
8771	4 432067373	AA491188	ESTs	other
22193	4 4169610024	R53891	Homo sapiens mRNA from chromosome Sq21-22 clone AJA	other
7896	4 4066170674	AA263032	ESTs	other
19902	4 3886145805	H66736	ESTs	other
9276	4 3668095209	D62374	ESTs	other
10716	4 3784529066	AA053319	ESTs	TM
13193	4 3751913512	AA442763	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]	other
5680	4 3723058417	X17620	NUCLEOSIDE DIPHOSPHATE KINASE A	other
35102	4 37147138	AA371509	EST - RC_AA371509	TM
17983	4 3612985487	AA189226	ESTs	other
24962	4 3497200925	AFPK-HUMTFRM11507	AFPK-HUMTFRM11507_5	?
31680	4 3410539609	N74438	ESTs	other
27168	4 330508894	AA410258	ESTs	other
28731	4 3231846659	D20981	EST	?
28348	4 3212284906	AA608752	ESTs	other

FIGURE 8 (cont.)

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16335	4	3019901487	AA018587	ESTs Weakly similar to III ALU SUBFAMILY SP WARNING ENTRY III [H.sapiens]	?
33036	4	2915644973	W48580	ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]	other
30180	4	2697721925	N33144	ESTs	other
35591	4	2895541242	AA401758	ESTs Weakly similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]	SS,
25340	4	2721717135	AA064554	EST	?
28106	4	2658103748	AA485084	ESTs	other
38690	4	2649184307	AA800121	ESTs	other
20203	4	2626499431	N26855	ESTs Moderately similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]	other
10251	4	2608700094	R76185	ESTs Weakly similar to CO1H6.7 [C.elegans]	SS,
12084	4	2604192389	AA417658	ESTs	SS,
31636	4	2509469427	N73680	Natural resistance-associated macrophage protein 2	TM
20769	4	2479765348	N67277	ESTs	other
1572	4	2353281083	K01834	EST - K01834	?
10923	4	2292322072	AA110036	ESTs	other
34380	4	2283782392	AA252414	ESTs	other
10132	4	2222816115	R35733	EST - R35733	other
16629	4	2161752119	AA036811	ESTs	other
25146	4	1969683794	AA026355	ESTs	?
28730	4	1965943098	D20959	ESTs Moderately similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]	other
10200	4	1874912391	R64521	ESTs	other
38695	4	1545784603	AA600176	ESTs	other
31365	4	150549878	N67550	ESTs	other
42379	4	1496120668	W37999	ESTs	other
28050	4	1428703354	AA479139	Acid phosphatase 1 soluble	other
2620	4	1386565707	M29474	Human recombination activating protein (RAG-1) gene complete cds	?
6927	4	1340593744	AF008442	Homo sapiens RNA polymerase I subunit RPA39 mRNA complete cds	other
13379	4	1269549188	AA449741	ESTs Weakly similar to AF-6 PROTEIN [H.sapiens]	other
5134	4	1218251808	U78293	Human clone 23948 mRNA sequence	other
2625	4	12113948	M26581	Zinc finger protein 8 (clone HF.18)	other
38005	4	1160483668	AA479969	ESTs	other
38575	4	1127196584	AA431085	EST	?
18296	4	1121837207	AA213620	ESTs Weakly similar to putative p150 [H.sapiens]	?
29531	4	1111458313	H88953	EST - RC_H88953	TM
143	4	1095880506	AFFX_HUMTFRRM11507_5	AFFX-HUMTFRRM11507_5	?
10970	4	0967613396	AA129390	ESTs	other
25836	4	0952825397	AA152305	Interferon (gamma)-induced cell line protein 10 from	SS,
19735	4	0937927853	H53038	EST	?
40711	4	0909708431	N53584	ESTs	other
4149	4	0901471427	U28386	RAG (recombination activating gene) cohort 1	TM
5767	4	0862784557	X53793	MULTIFUNCTIONAL PROTEIN ADE2	other
5503	4	0861035825	X05232	Sironelysin	SS
20310	4	0841711856	N34893	ESTs Highly similar to HYPOTHETICAL 47.8 KD PROTEIN B0283.9 IN CHROMOSOME III [Caenorhabditis elegans]	other
456	4	0599824566	D38145	Prostaglandin I2 (prostacyclin) synthase	SS,
7814	4	0559685576	AA248406	ESTs	other
40230	4	0447282719	H90161	ESTs	SS
33651	4	039204804	W95408	ESTs	other
16777	4	0231657929	AA048968	EST	?
19110	4	0094905222	H08778	ESTs	other
34442	4	0077010365	AA258093	HCR-T1	other
5099	4	004992433	U79247	Human clone 23599 mRNA sequence	TM

FIGURE 8 (cont.)

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8209	3 9990473163	AA384223	ESTs	other
24408	3 9976580074	V90145	ESTs	other
26596	3 9974918787	AA278943	ESTs	other
16485	3 9611264008	AA026269	Screen focus forming virus (SFFV) proviral integration oncogene ccl1	other
32959	3 9804901745	W42451	ESTs	TM
27005	3 9799768093	AA398695	ESTs Weakly similar to ED4F6 2 gene product [C. elegans]	other
21809	3 9526765967	N21043	EST	?
9596	3 9440163451	H91564	ESTs	TM
29024	3 8377933930	F09315	Homo sapiens mRNA for KIAA0563 protein partial cds	other
71694	3 0356365684	R39317	Homo sapiens protein-tyrosine kinase EPHB2v (EPH82) mRNA complete cds	other
13207	3 829998104	AA443321	ESTs	other
37865	3 9143752629	AA476023	ESTs Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]	other
36201	3 9128828172	AA421164	ESTs	?
8961	3 8981180269	AFFX-HUMITFRRM11507	AFFX-HUMITFRRM11507_3	?
17444	3 8927133917	AA115933	ESTs	other
25869	3 8919834527	AA157287	ESTs Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZYG86.3 IN CHROMOSOME B1 [Caenorhabditis elegans]	TM
24862	3 89042252	Z41415	ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]	other
26885	3 889063205	AA281950	ESTs	?
42300	3 8850230368	T95850	ESTs	?
6495	3 8830844863	X32715	Zinc finger protein 74 (Cos52)	other
39604	3 8828045942	AA588803	ESTs	TM
36358	3 8826713718	AA425758	ESTs	other
30560	3 8732764451	N49284	MYB PROTO-ONCOGENE PROTEIN	other
14413	3 8724486158	AA800150	ESTs	other
23823	3 8574824967	T91805	Homo sapiens mRNA for ST1C2 complete cds	other
38158	3 8530968938	AA487021	EST	?
2572	3 8518747554	M27281	Vascular endothelial growth factor	other
40100	3 8464168967	H75933	Laminin receptor (2H5 epitope)	other
40258	3 8462922993	H93340	ESTs	TM
20944	3 8461621525	H74443	ESTs	other
20411	3 8459400966	N48963	Homo sapiens mRNA for KIAA0689 protein partial cds	other
10345	3 8457714481	AA001663	ESTs	other
31261	3 8451974374	H56248	EST	other
6513	3 8378410994	AA446990	ESTs	other
13877	3 8363409835	AA476504	ESTs	other
40748	3 8253562321	H56879	EST	?
14509	3 8152852163	AA609943	ESTs	other
10281	3 8065567331	R80333	ESTs	other
25284	3 8044158642	AA045074	ESTs Weakly similar to 52-kD SS-A/Ro autoantigen [H. sapiens]	other
6730	3 7900025129	Y09305	H. sapiens mRNA for protein kinase Dyrk4 partial	other
16033	3 7884582402	AFFX-HUMISGF3AM97935	AFFX-HUMISGF3AM97935_M8	?
38242	3 7827164808	AA621523	ESTs	other
27354	3 7794760435	AA425221	ESTs	?
4552	3 777263605	U49188	Human placenta (Df(3)) mRNA complete cds	SS, TM
18385	3 7756189108	AA227219	Homo sapiens CAGF9 mRNA partial cds	other
16754	3 7677416053	AA046067	EST - RC_AA046067	other
12752	3 7671137403	AA421250	ESTs	other
42463	3 7601033100	W50180	ESTs	other

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10614	3 7581089016	AA037357	ESTs	?
867	3 7459337969	D87718	Human mRNA for KIAA0007 gene partial cds	other
7608	3 7336047135	AA180907	ESTs	other
31795	3 732738742	N80703	ESTs	other
35377	3 7273784603	AA399453	EST - RC_AA399453	?
27828	3 7243928524	R98192	ESTs	other
25240	3 7243198335	AA039713	ESTs	other
11008	3 7197391365	AA194289	ESTs Weakly similar to ASH1 [D.melanogaster]	?
4341	3 7162349944	U38545	Human ARF-activated phosphatidylcholine-specific phospholipase D1a (NPLD1) mRNA complete cds	other
28833	3 7147818393	D59787	EST - RC_D59787_1	?
3750	3 7121007154	U09279	Collagen type XIX alpha 1	SS,
17483	3 6943413512	AA122147	ESTs	TM
16854	3 6915208471	AA055552	ESTs Weakly similar to KIAA0319 [H.sapiens]	TM
3709	3 6891556771	U07550	Heat shock 10 kD protein 1 (chaperonin 10)	other
1808	3 6852978422	L00205	KERATIN TYPE II CYTOSKELETAL 6D	?
24577	3 6617721053	Z38727	Homo sapiens mRNA for KIAA0555 protein complete cds	TM
31032	3 6570916386	N52508	ESTs	other
4951	3 6536195433	U69546	Human RNA binding protein Etr-3 mRNA complete cds	other
37660	3 6523275307	AA460225	ESTs	other
20418	3 6495357091	N49209	ESTs	other
27895	3 6485167436	AA470155	Homo sapiens coatomer protein (COPa) mRNA complete cds	?
7971	3 6434397185	AA287423	ESTs	other
27606	3 64303453	AA443793	ESTs	other
24677	3 6427250633	Z39338	ESTs Highly similar to POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR [Mus musculus]	other
11070	3 6406198277	AA148521	ESTs Weakly similar to putative p150 [H.sapiens]	TM
9328	3 6356048599	D69618	Homo sapiens importin-alpha homolog (SRP1 gamma) mRNA complete cds	other
36826	3 634589802	AA435995	ESTs	other
17878	3 6300045785	AA134275	Human HIV1 tat element regulatory factor mRNA sequence from chromosome 3	other
36209	3 6274594477	AA421256	ESTs Weakly similar to LIS-1 protein [H.sapiens]	other
34120	3 6258090412	AA211815	EST	?
39152	3 6246442011	AA486737	H.sapiens mRNA for Sm protein F	TM
38463	3 6184693268	AA504491	ESTs Weakly similar to contains similarity to C3HC4-class zinc finger [C.elegans]	TM
20064	3 6183899978	H98653	ESTs	TM
31256	3 5992620732	N56152	EST	?
9713	3 5985228643	L44338	Homo sapiens mRNA for KIAA0525 protein partial cds	other
28622	3 5788056147	D11837	ESTs	?
38057	3 5736105703	AA481549	EST - RC_AA481549	other
28763	3 5688723791	D45568	EST	?
16996	3 5680705709	AA069038	EST - RC_AA069038	TM
28628	3 5604144617	D11888	ESTs Moderately similar to PROHIBITIN [H.sapiens]	?
25804	3 5442954572	AA148885	ESTs	?
2492	3 5423984239	M22898	Tumor protein p53 (Li-Fraumeni syndrome)	?
14904	3 5411970737	T83389	ESTs Highly similar to GEPHYRIN [Rattus norvegicus]	other
25265	3 5347588502	AA043765	H.sapiens RY-1 mRNA for putative nuclear acid binding protein	other
13605	3 5327912417	AA456437	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]	other
42307	3 5318436465	T96595	EST - RC_T96595	TM
1544	3 526202414	J05068	TRANSCOBALAMIN I PRECURSOR	SS,
42339	3 5195081035	W02072	ESTs Weakly similar to No definition line found [C.elegans]	other
42311	3 5183719631	T97257	ESTs	other
2023	3 5040279423	L34600	INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR	other

FIGURE 8 (cont.)
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4540	3 4955306569	U48807	Human MAP kinase phosphatase (MKP-2) mRNA complete cds	other
33707	3 4888534277	Z39297	Neuronal pentraxin II	other
17220	3 4755703461	AA083070	EST - RC_AA083070_s	SS
24332	3 4725273806	V65782	ESTs	other
35897	3 4660663718	AA412067	ESTs	other
20158	3 4538150065	N23638	ESTs Weakly similar to coded for by C. elegans cDNA y652e10.5 (C. elegans)	other
8338	3 4485832071	AA417152	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	other
387	3 4421427234	D28589	EST - D28589	other
12319	3 4356269717	AA398109	ESTs	SS, TM
38276	3 4313139432	AA489711	ESTs	TM
15643	3 4312194246	V58247	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]	other
11218	3 4232832843	AA180488	ESTs	TM
16539	3 4178863379	AA029328	Human mRNA for KIAA0073 gene partial cds	?
26203	3 4162847487	H28581	ESTs	other
13838	3 4162403464	AA465342	ESTs	other
25565	3 4160353003	AA112389	H4(D10517C)	SS
34018	3 4145335883	AA181488	Human high-affinity copper uptake protein (HCTR1) mRNA complete cds	TM
251	3 4006042851	D14520	Basic transcription element binding protein 2	other
3778	3 4004518201	U08848	Zinc finger protein 139 (clone pHZ-37)	other
24535	3 3964397837	Z38409	ESTs	other
18858	3 3925184041	AA065759	Human mRNA for KIAA0128 gene partial cds	TM
16127	3 3921645927	AA004669	ESTs	other
36683	3 3841316491	AA432268	ESTs	other
26149	3 3809497785	AA250824	ESTs Weakly similar to ZINC FINGER PROTEIN 81 [H. sapiens]	other
4011	3 3758093471	U20536	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds	other
41001	3 3794250205	N78844	ESTs	other
5660	3 3789306731	X18396	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE	SS
19204	3 3776332343	H11829	ESTs	other
42323	3 3768515879	T98152	Fibrin 2	SS
28928	3 3725378868	AA342580	ESTs	SS
20497	3 369285912	N52565	ESTs	other
19226	3 36674249	H12455	ESTs	other
36267	3 3606841839	AA424045	ESTs	other
32257	3 359796018	R54726	DNA-REPAIR PROTEIN XRCC1	other
17365	3 3522214732	AA101651	ESTs	other
15296	3 3491193196	V16684	ESTs Moderately similar to Similar to S. cerevisiae hypothetical protein L3111 [H. sapiens]	other
17675	3 3485872272	AA134064	ESTs	TM
40332	3 3458489589	H97585	Homo sapiens mRNA from chromosome 6q21-22 clone A3-A	other
7219	3 3385684843	AA056319	Homo sapiens protein phosphatase 2A B56-epitope (PP2A) mRNA complete cds	other
10006	3 3322827822	N81193	Homo sapiens mRNA for KIAA0628 protein complete cds	?
33985	3 3276877441	AA181580	Homo sapiens importin beta subunit mRNA complete cds	other
8570	3 3263855302	H85169	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene complete cds	other
37551	3 3155406577	AA456679	ESTs	other
606	3 3111782759	D88613	Human mRNA for hGCMs complete cds	other
23650	3 3069426629	T86293	ESTs	other
18367	3 3007433533	AA224180	ESTs Moderately similar to ovarian-specific protein [H. norvegicus]	?
42494	3 2908070546	V89385	H. sapiens HMAA gene (Clone T33)	other
14310	3 2753564661	AA588412	ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PHB-PCY1 INTERGENIC REGION [Saccharomyces cerevisiae]	SS, TM

FIGURE 8 (cont.)

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19233	3 274416299	H12634	ESTs	other
42263	3 2731066284	T84343	Homo sapiens M062 protein spliced isoform 2 mRNA complete cds	other
12909	3 271352097	AA424405	ESTs	other
36385	3 26960223617	AA424469	ESTs	other
21555	3 2666266446	R33073	EST	?
13767	3 2656595616	AA463234	ESTs	TM
4738	3 2661591937	U58766	Human FX protein mRNA complete cds	other
7258	3 263106866	AA075427	ESTs	other
17041	3 2629042076	AA070364	EST - RC_AA070364	?
15504	3 2615745245	V28362	ESTs	other
23793	3 2611829896	T90971	EST - RC_T90971	other
18214	3 2572346955	AA196533	ESTs	TM
7401	3 257164123	AA094800	Human translation initiation factor eIF3 p58 subunit mRNA complete cds	other
18912	3 2553600001	F10913	Homo sapiens clone 23617 unknown mRNA partial cds	other
36317	3 2509495347	AA425089	Human mRNA for KIAA0334 gene complete cds	?
9410	3 250727851	H20443	Hsapiens mRNA for TRES	other
2146	3 2464307896	L41390	EST - L41390	?
10663	3 240614336	F04258	ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Box trunus]	?
33891	3 2392191406	AFFX-HUMTFRM11507	AFFX-HUMTFRM11507_M	?
14435	3 2372161315	AA068730	ESTs Weakly similar to ELONGATION FACTOR 1-ALPHA [Glandia intransitella]	other
9584	3 2363829855	H88128	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]	other
22061	3 2340096572	R49218	ESTs	TM
35798	3 233287605	AA410223	EST - RC_AA410223	?
37403	3 2261852043	AA453613	ESTs	other
15796	3 2260359988	X16889	ALPHA-GALACTOSIDASE A PRECURSOR	SS
15840	3 2257832439	X70944	PTB-ASSOCIATED SPLICING FACTOR	other
7518	3 2232170427	AA147144	EST - AA147144	other
32335	3 2228388982	R78248	ESTs	other
3258	3 2180538038	M92439	130 KD LEUCINE-RICH PROTEIN	other
4400	3 2173696081	U41387	Human Gu protein mRNA partial cds	other
7681	3 2074414299	AA206983	Homo sapiens mRNA for DRIM protein	other
16678	3 2041209443	W68649	ESTs	TM
39590	3 2038953621	F08281	ESTs	other
26483	3 1980022253	AA291821	ESTs Weakly similar to putative p150 [H.sapiens]	?
9808	3 1920380384	N80627	Transcription factor 12 (HTF4 helix-loop-helix transcription factors 4)	other
27755	3 1900699454	AA453444	ESTs	other
29983	3 1882290623	N26011	ESTs	?
21350	3 1876957756	R15846	ESTs	other
11881	3 1870525747	AA280328	ESTs	other
23930	3 1817500097	T06690	ESTs Weakly similar to H ¹ ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	other
30399	3 1792054412	N45228	EST	?
22266	3 1781990049	R59312	ESTs	other
13494	3 1673900969	AA453431	ESTs	TM
12908	3 1530533441	AA427579	ESTs	other
22319	3 1469419301	R60567	ESTs	TM
31309	3 1466750523	N66818	ESTs	TM
31192	3 1458779823	N64406	ESTs	other
11288	3 144853134	AA196512	ESTs	TM
170	3 1430726349	D00596	Thymidylate synthase	?
5307	3 1347905628	U90549	Human non-histone chromosomal protein (HNC) mRNA complete cds	other

FIGURE 8 (cont.)

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26105	31311103325	AA243133	Homo sapiens serine/threonine kinase (STAK) mRNA complete cds	other
11659	31281785108	AA251909	Homo sapiens MAD3-like protein kinase mRNA complete cds	other
19177	3124408365	K10984	ESTs	TM
8389	31241545074	AA425230	ESTs	TM
34087	31216555797	AA205125	Protein serine/threonine kinase stg2	other
25001	31209327466	AA004718	ESTs Weakly similar to BAP31 protein [H.sapiens]	other
14149	31198500308	AA489665	ESTs	other
10167	31191980323	R55076	ESTs	other
17390	31071055868	AA102508	ESTs	other
42397	31044680628	V42028	ESTs	other
14835	31042015743	T94828	ESTs Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]	other
41873	31030349819	R78618	ESTs Weakly similar to GTP-binding protein rab10 [R.norvegicus]	other
2750	31026223619	M35999	Integrin beta 3 (platelet glycoprotein Ila antigen CD61)	?
3190	31025223619	M86808	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT TESTIS-SPECIFIC FORM PRECURSOR	?
17406	30999394188	AA112979	Homo sapiens mRNA for VRK1 complete cds	other
598	30912414004	D59253	Homo sapiens mRNA for low molecular mass ubiquitin-binding protein complete cds	other
29348	30802365759	H69021	ESTs	other
14130	30744457534	AA489041	ESTs	other
14134	3069660341	AA489090	ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]	other
42421	30684159011	V45491	ESTs Weakly similar to T23G11.7 [C.elegans]	other
15723	30680746209	V79060	ESTs Highly similar to ribosome-binding protein p34 [R.norvegicus]	other
11140	30650815198	AA158132	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]	other
28531	30649767987	C20679	ESTs	other
2021	30629707497	L34409	Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment	?
14322	3058260163	AA810108	ESTs Highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.05C [Schistosoma haematodes pombae]	SS,
29853	30545621815	N22162	ESTs	other
15962	30521475703	Z21420	ESTs	other
6541	30509806038	X95632	Human Abi Interactor 2 (Abi-2) mRNA complete cds	other
13229	30485366337	AA443811	ESTs	other
27315	3048622812	AA424038	ESTs	other
13621	30302305369	AA456821	ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]	other
35329	30269182406	AA412429	ESTs	other
17925	30253428426	AA184209	Homo sapiens RRM RNA binding protein GRY-top (GRY-RSP) mRNA complete cds	other
5053	30249536782	U76992	Human Tat-SF1 mRNA complete cds	other
15080	30213293848	U54999	Human LGN protein mRNA complete cds	other
17757	30205801351	AA147224	EST	?
19050	30192378314	H05509	ESTs	other
26530	30176823278	AA278650	ESTs	other
16806	30158779932	AA053258	Homo sapiens mRNA for KIAA0648 protein partial cds	TM
29088	30149440394	F13700	Homo sapiens ribonuclease P protein subunit p40 (RPP40) gene complete cds	other
22960	30141662421	T10272	ESTs	other
33585	30121672451	V93000	ESTs	other
220	30109180714	D13627	Human mRNA for KIAA0002 gene complete cds	TM
4298	30024671064	U36448	Human Ca2+-dependent activator protein for secretion mRNA complete cds	TM
7445	29995643641	AA104023	ESTs	?
40903	29980347088	N68670	ESTs	?
18055	29973386648	AA176387	ESTs	other
7282	29962782596	AA063339	ESTs	other

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9348	2 9949017671	H03680	ESTs	TM
806	2 9877476515	D87009	Human (lambda) DNA for immunoglobulin light chain	?
38447	2 9876031644	AA504255	Human protein kinase ATR mRNA complete cds	other
41484	2 9870604981	R46837	ESTs	?
9682	2 9869352305	L19181	TRANSLATIONAL INITIATION FACTOR 2 GAAMBA SUBUNIT	other
16978	2 9801154057	AA083625	EST	?
37428	2 9756408909	AA454016	ESTs	other
2588	2 9725698298	M27878	Zinc finger protein 84 (MPF2)	other
15174	2 9695024379	U62987	Human Bcl-2 binding component 3 (bbc3) mRNA partial cds	other
33620	2 9657446567	W93943	ESTs	other
6784	2 9655061112	Y11581	Homo sapiens ribosomal protein S12 gene nuclear gene encoding mitochondrial protein complete cds	?
41077	2 9642389716	N95028	ESTs	TM
1932	2 9609985996	L24804	Human (p23) mRNA complete cds	other
98556	2 9588964022	F03738	ESTs	other
16108	2 9574232912	AA002258	ESTs	SS
32156	2 9574232912	R40381	ESTs	?
13617	2 9552306838	AA456646	ESTs	other
11899	2 955203991	AA281251	ESTs Weakly similar to Inthorax protein trxtl [D.melanogaster]	other
6056	2 947654132	X58194	Pancreothym (human keratinocyte line HaCat) mRNA 2105 nt	TM
15446	2 9445456286	W27374	Homo sapiens 10kD protein (BC10) mRNA complete cds	other
38086	2 9445277834	AA482557	EST	?
13878	2 9444133384	AA476604	ESTs	other
6209	2 9422425032	X78770	H.sapiens PAP mRNA	other
358	2 9357591919	D28791	Phosphatidylinositol glycan class A (paroxysmal nocturnal hemoglobinuria)	?
1351	2 9266145582	HG4755-HT5203	EST - HG4755-HT5203	?
42824	2 9266145582	W87804	ESTs	other
34895	2 9242794509	AA311872	ESTs	other
20157	2 9214162978	N23393	ESTs	other
29248	2 9188102155	H52918	ESTs	?
4893	2 9178533564	U66615	Human SVM/SNF complex 155 KDa subunit (BAF155) mRNA complete cds	other
10104	2 9150324884	R23855	ESTs	TM
15035	2 9147218324	U46116	Protein tyrosine phosphatase receptor type gamma polypeptide	?
1605	2 9141775797	L00058	V-myc avian myelocytomatosis viral oncogene homolog	?
4536	2 9075603336	U48705	Receptor protein-tyrosine kinase EDDR1	?
10173	2 905710598	R56878	ESTs Weakly similar to cell division control protein CDC21 [H.sapiens]	?
26555	2 9056210172	AA279071	ESTs Weakly similar to T08A11.2 [C.elegans]	other
4401	2 9047655582	U41515	Human deleted in split hand/split foot 1 (DSS1) mRNA complete cds	other
21009	2 8995011918	N90401	ESTs	TM
3602	2 894817322	U01317	HEMOGLOBIN EPSILON CHAIN	?
4833	2 8919254016	U63455	Sulfonylurea receptor (hyperinsulinemia)	?
38200	2 8912301426	AA421164	ESTs	?
26645	2 8898309441	AA281076	ESTs	other
35299	2 8887661574	AA396622	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)	other
9804	2 8880347344	M74558	Human SIL mRNA complete cds	other
5216	2 8877977815	U83410	Human CUL-2 (cul-2) mRNA complete cds	other
12313	2 8847621603	AA397816	ESTs	other
5928	2 8636060438	X62048	WEE1-LIKE PROTEIN KINASE	?
39586	2 8618258313	F09155	ESTs	TM
34758	2 8775214637	AA287880	EST	?
18189	2 8763949024	AA195318	ESTs	other

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10867	2 8720974689	H81476	ESTs	?
6061	2 8678372836	X59396	CD47 antigen (Rn-related antigen integrin-associated signal transducer)	SS, TM
5254	2 862067239	U86782	Human 26S proteasome-associated pad1 homolog (PDH1) mRNA complete cds	other
13579	2 8570620494	AA455967	Human neuronal PAS2 (NPAS2) mRNA complete cds	?
11117	2 8568053461	HG3075-HT3236	EST - HG3075-HT3236	?
20533	2 8564678641	N54407	ESTs	TM
38495	2 8562453397	AA505118	Human nucleoporin 98 (NUP98) mRNA complete cds	other
33729	2 8548155651	Z39654	EST	?
2028	2 8532778139	L35035	RIBOSE 5-PHOSPHATE ISOMERASE	other
27374	2 8520674335	AA425816	ESTs Weakly similar to Y53C12A.3 [C.elegans]	other
19404	2 8518690748	H20068	ESTs	other
26108	2 8504706329	AA243189	ESTs	SS,
4189	2 8439972255	U30930	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)	TM
16708	2 8427388072	AA043944	ESTs	other
357	2 8350474214	D26156	Human mRNA for transcriptional activator hSNF2b complete cds	other
26045	2 8316740098	AA236276	ESTs	other
17796	2 8312342777	AA150435	ESTs	other
8059	2 8268722809	AA310967	ESTs Weakly similar to T04AB.11 [C.elegans]	other
42914	2 827999584	N69220	ESTs	other
27169	2 8263163852	AA410287	H. sapiens mRNA for basic transcription factor 2.34 kD subunit	other
21358	2 8262413945	R16079	ESTs	other
3572	2 8261469131	S87759	Protein phosphatase 2C alpha (human testicular tumor mRNA Z346 nt)	other
11877	2 8259099942	AA262727	ESTs	other
1653	2 8234017508	L05424	CD44 antigen (cell adhesion molecule)	?
24645	2 8131264428	Z39106	ESTs	other
35830	2 8126257031	AA411448	ESTs	TM
4433	2 8114422177	U43279	EST - U43279	?
20151	2 8109454503	N22895	Homo sapiens clone 1400 unknown protein mRNA partial cds	other
36548	2 8084431065	AA599267	EST - RC_AA599267	other
7777	2 8071817829	AA236820	ESTs	other
32845	2 80583194	VQ31568	EST	?
28258	2 8043934182	AA505133	ESTs	other
6853	2 798263202	Z22851	TRANSCRIPTION FACTOR P65	?
35944	2 7913872996	AA412483	ESTs	?
30648	2 7866522676	N50971	ESTs	?
18365	2 7857482775	H01411	ESTs	TM
8816	2 785444221	AA460077	ESTs	other
14945	2 7838257917	T99606	ESTs Weakly similar to F35G2.2 [C.elegans]	other
8375	2 7805657722	AA422160	H.sapiens NAP (nucleosome assembly protein) mRNA complete cds	other
34926	2 7792111121	AA342084	EST - RC_AA342084	other
320	2 7786978435	D21282	Human mRNA for KIAA0035 gene partial cds	other
27057	2 7781218063	AA400998	ESTs	SS,
36282	2 7748002184	AA424513	EST - RC_AA424513	other
6480	2 7735431318	X91788	H. sapiens mRNA for lcn protein	other
15424	2 7731675808	W27054	APOLIPOPROTEIN A1 REGULATORY PROTEIN-1	other
11802	2 7730818255	AA243007	ESTs	?
18175	2 77056686	AA194730	ESTs	?
25202	2 7698585998	AA034527	EST	?
1581	2 7697545972	L07493	Replication protein A (E. coli RecA homolog RAC51 homolog)	other
14568	2 767884858	AA621122	ESTs	other
25814	2 7633374335	AA115769	ESTs	other

FIGURE 8 (cont.)

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14187	2.7606046934	AA490825	ESTs	other
31599	2.7591187858	N72196	EST	other
18253	2.7471964081	AA208370	ESTs	other
6193	2.7442487702	X76092	Regulatory factor (trans-acting) 3	other
22911	2.7433449859	T03865	ESTs	other
35540	2.7432465006	AA401274	Homo sapiens RRM RNA binding protein GRY-100 (GRY-RBP) mRNA complete cds	other
35955	2.7389431758	AA412528	ESTs Weakly similar to DRF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH (R nonviral)	other
17642	2.7377607284	AA132693	ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC (H sapiens)	other
6131	2.7371784571	X72841	Human retinoblastoma-binding protein (RbAp48) mRNA complete cds	other
41429	2.7347564467	R44994	ESTs	other
17052	2.7323944161	AA070815	EST - RC_AA070815	other
34243	2.7294147034	AA235050	ESTs	?
22937	2.7284347248	T10065	Homo sapiens TLS-associated protein TASR-2 mRNA complete cds	other
5183	2.7243199196	U82130	Human tumor susceptibility protein (TSG101) mRNA complete cds	other
30837	2.7231409239	N54416	ESTs	other
16243	2.7228028265	AA012902	ESTs	TM
19954	2.7215183485	H80100	ESTs	other
6444	2.720441384	X89760	H.sapiens mRNA for TGF protein	other
5916	2.7192579481	X51072	Human mRNA for T cell receptor clone IGRA17	SS,
6240	2.7168544194	X78627	H.sapiens mRNA for transt	?
42116	2.7144176166	T59924	EST - RC_T59924	other
7701	2.7107290468	AA215333	ESTs	TM
17568	2.7096978968	AA128905	ESTs	TM
42534	2.7086014274	W73189	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	SS, TM
29813	2.708372123	N21111	ESTs	other
36898	2.7067394943	AA609458	ESTs	other
10318	2.7055635457	R88880	ESTs Moderately similar to zinc finger protein (M. musculus)	other
14789	2.7040621985	S54641	HZF-16	other
32961	2.7012195407	W38366	Human mRNA for KIAA0005 gene complete cds	other
35273	2.6975345483	AA398507	ESTs	other
10180	2.6960696303	R50100	ESTs	?
32563	2.6955482902	T27697	Human mRNA for KIAA0036 gene complete cds	other
34502	2.6948574449	AA262768	ESTs	TM
13223	2.6912995353	AA443720	ESTs	other
8494	2.6906515739	AA443460	ESTs	other
7776	2.6900717525	AA236771	ESTs	other
10400	2.6898958951	AA007234	ESTs	other
1130	2.6897527619	HG3132-HT3308	EST - HG3132-HT3308	?
2379	2.6874247447	M16937	Human homeo box c1 protein mRNA complete cds	TM
18906	2.6861450774	F10868	Human SH3 domain-containing protein SH3P18 mRNA complete cds	?
34796	2.6853510115	AA291259	ESTs	TM
41955	2.6821408177	T33311	Neuronal pentraxin II	other
2009	2.6791061739	L33881	Protein kinase C iota	?
33688	2.6775081286	Z38501	ESTs Weakly similar to PROBABLE ES PROTEIN [Human papillomavirus type 58]	other
1385	2.6771402807	HG884-HT884	EST - HG884-HT884	?
24758	2.6750080868	Z40075	ESTs	other
7620	2.6742248913	AA192484	ESTs Weakly similar to MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 (S. cerevisiae)	other
30733	2.6739544406	N52078	Homo sapiens mRNA for KIAA0637 protein complete cds	other
21256	2.6723253055	R09195	Homo sapiens mRNA for KIAA0564 protein partial cds	other
40526	2.669020458	N29325	ESTs Highly similar to 47 KD PROTEIN (Pseudomonas	other

FIGURE 8 (cont.)

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			chloroplasts]		
25285	2 6685455406	AA045083	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	other	
9296	2 667949532	D82776	ESTs Weakly similar to unknown [S cerevisiae]	SS	
12174	2 6669305328	AA282128	ESTs	other	
38357	2 6652770538	AA491285	EST	TM	
3154	2 6619596800	M83712	Cholinergic receptor nicotinic alpha polypeptide 5	TM	
7383	2 655440738	AA038834	ESTs Weakly similar to HYPOTHETICAL 16.8 KD PROTEIN IN SMY2-RPS101 INTERGENIC REGION [S cerevisiae]	other	
1923	2 6530372325	L23808	Metalloproteinase 12 (macrophage elastase)	SS	
24908	2 6527048053	Z41840	ESTs	other	
34726	2 6495430564	AA287278	ESTs	SS	
30407	2 6495430564	N45983	ESTs	TM	
20408	2 6450891347	N48787	ESTs Moderately similar to III ALU SUBFAMILY SC WARNING ENTRY III [H sapiens]	other	
7158	2 6455059455	AA037208	ESTs	TM	
26286	2 6445109706	AA253351	ESTs	?	
19822	2 6431968212	H58684	ESTs	?	
12379	2 6428182941	AA399418	Homo sapiens mRNA for JN23 protein complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110133Q7 (RZPD Berlin))	other	
22698	2 6396306055	R89287	ESTs	other	
24161	2 6394502284	W58015	ESTs	other	
9558	2 6370149706	H81497	ESTs	TM	
18104	2 6358767288	AA188801	ESTs	other	
24882	2 6357248889	Z41563	ESTs	other	
40038	2 6347874784	H59485	ESTs	other	
8965	2 6344845492	AB002359	Human mRNA for KIAA0361 gene KIAA0361 protein	other	
22148	2 6288326966	R51831	ESTs	other	
4627	2 6277060831	U51990	Human hPtp18 mRNA complete cds	other	
8394	2 6275394634	AA426156	ESTs	TM	
20422	2 6272599718	N49300	ESTs	other	
41602	2 6258613824	R57258	ESTs Moderately similar to moesin [M musculus]	other	
612	2 6257836582	D63480	Human mRNA for KIAA0146 gene partial cds	TM	
4621	2 619521444	U82801	Human protease M mRNA complete cds	SS, TM	
16807	2 617722828	AA053296	ESTs	other	
15288	2 6173997018	W07582	ESTs Moderately similar to rAB [R norvegicus]	other	
38023	2 6135617291	AA481058	ESTs	other	
23822	2 6120077647	T91715	ESTs Highly similar to HYPOTHETICAL 103.6 KD PROTEIN IN COX5B-PFK26 INTERGENIC REGION [Saccharomyces cerevisiae]	TM	
10951	2 6116018519	AA126719	ESTs	other	
6150	2 6113980879	X74262	RETINOBLASTOMA BINDING PROTEIN P48	other	
39336	2 6109987712	C20945	ESTs Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC8 INTERGENIC REGION [Saccharomyces cerevisiae]	other	
17793	2 6102158176	AA150242	ESTs Highly similar to modulator recognition factor 2 [H sapiens]	other	
26891	2 6085107387	AA292559	ESTs	other	
2175	2 607468578	L42621	Homo sapiens L y-9 mRNA complete cds	TM	
10642	2 6048724507	AA040149	Human Chromosome 16 BAC clone CIT987SK-A-270G1	other	
15026	2 6031453392	U41816	Human C-1 mRNA complete cds	other	
7659	2 6019047419	AA215299	Homo sapiens chromosome 19 cosmid R30763	other	
6543	2 6011828937	X95654	Homo sapiens mRNA for SCP-1 complete cds	other	
20636	2 5992884878	NG2122	ESTs	other	
11308	2 5993311375	AA271114	ESTs	other	
4086	2 5966362866	U24704	Human antisecretory factor-1 mRNA complete cds	other	
38815	2 5963996726	AA598938	EST - RC_AA598938	other	
11819	2 5961501969	AA258186	ESTs	other	

FIGURE 8 (cont.)

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37433	2.5957446266	AA454103	ESTs	other
28270	2.5939657529	AA521186	ESTs	TM
5587	2.5932338399	X13482	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'	other
19041	2.5930132063	H59517	ESTs Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD (<i>Drosophila melanogaster</i>)	other
10655	2.5925442731	AA040882	ESTs	?
14053	2.5899324577	AA485147	ESTs Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 BY CHROMOSOME III (<i>Caenorhabditis elegans</i>)	other
31574	2.5883094453	N71303	EST	?
7614	2.5870699315	AA187579	ESTs Weakly similar to Yel007c-ap (<i>S. cerevisiae</i>)	other
37671	2.5847445397	AA479195	EST	?
7090	2.5845365105	AA099913	Human sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds	other
17852	2.5841100415	AA156360	ESTs	other
24219	2.5823376094	W69980	ESTs	other
19070	2.5813645258	H05970	Human clone Z3960 mRNA sequence	other
17719	2.5803606155	AA136569	EST	?
38669	2.5791967991	AA599694	Human mRNA for KIAA0133 gene complete cds	TM
20982	2.5763957078	N79565	ESTs	TM
9158	2.5731838907	D31446	Human sapiens breakpoint cluster region protein 1 (BCRG1) mRNA complete cds	other
11362	2.5731137778	AA227261	ESTs	other
8613	2.5723119487	AA458555	Human sapiens mRNA for KIAA0546 protein partial cds	TM
13868	2.5715997844	AA476319	ESTs	SS,
10303	2.5712815907	R86178	Ataxia telangiectasia mutated (includes complementation groups A C and D) EST	?
22299	2.567916035	R59801	EST	?
18267	2.5673459605	AA200591	EST - RC_AA200591	other
20555	2.5654242508	N55168	ESTs	other
39552	2.5645918108	F03605	PUTATIVE 60S RIBOSOMAL PROTEIN	other
27530	2.5631130949	AA435996	ESTs	other
1795	2.5608471476	L13434	Human chromosome 3p21.1 gene sequence complete cds	?
14745	2.5603154956	D60354	Human mRNA for KIAA0007 gene partial cds	other
2993	2.5587815672	M64929	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform	other
19191	2.5545260975	H11297	ESTs	other
12986	2.5507999853	AA430032	ESTs Moderately similar to PTTG gene product (<i>R. norvegicus</i>)	?
15452	2.5488533884	W27451	Human Cdc5-related protein (PCDC5SRP) mRNA complete cds	other
16003	2.5465671712	AA171692	ESTs	other
24198	2.5461854497	W67524	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	TM
42653	2.5447626827	W92703	ESTs	other
26446	2.544106171	AA258798	EST Weakly similar to putative p150 (<i>H. sapiens</i>)	?
30438	2.5368548574	M47204	ESTs Weakly similar to C50F4.12 (<i>C. elegans</i>)	other
36365	2.5362912735	AA425823	ESTs Weakly similar to probable CBP3 protein homolog (<i>C. elegans</i>)	other
28135	2.535658968	AA243765	ESTs	other
41885	2.5349932888	T23449	ESTs Moderately similar to ZNF127-Xp (<i>H. sapiens</i>)	SS,
15457	2.5343495968	W27560	ESTs	other
27748	2.5320767519	AA453159	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds	other
32315	2.5302979959	R59840	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (<i>Nycticebus coucang</i>)	?
25310	2.5274401579	AA046745	ESTs	other
42720	2.5222453766	Z39436	ESTs	other
12939	2.5200945911	AA428204	ESTs	other
30746	2.5198420998	N52243	ESTs	other
2222	2.5183624578	L76703	Human sapiens protein phosphatase 2A B56-epsilon (PPP2A) mRNA complete cds	?
11809	2.5191765545	AA243303	ESTs	TM

FIGURE 8 (cont.)

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9658	2 5185814336	L16991	Deoxythymidylate kinase	other
12210	2 5172044681	AA293774	ESTs Weakly similar to PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE MITOCHONDRIAL (C elegans)	other
3563	2 5169818533	S83364	EST - S83364	other
42407	2 5128230047	V44768	Homo sapiens nephrin (NPHP1) mRNA partial cds	?
32826	2 5128052161	V20391	Human mRNA for kinesin-related protein partial cds	other
9692	2 5119977118	L37747	LAMIN B1	?
27862	2 5094571267	AA458908	ESTs	TM
33691	2 509287494	Z39630	EST	other
17288	2 5088624644	AA085178	ESTs	SS,
9888	2 5078170902	H35449	ESTs Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/ALP4-GVP1 INTERGENIC REGION (Saccharomyces cerevisiae)	other
5932	2 5073880985	X62153	Minichromosome maintenance deficient (S. cerevisiae)	other
15885	2 5053862932	X95073	H.sapiens mRNA for transin associated protein X	other
17952	2 5049193223	AA165677	ESTs Weakly similar to F16A11.1 (C elegans)	other
12187	2 5042458391	AA293206	ESTs	other
6210	2 5042034458	X78942	Homo sapiens golgin-245 mRNA complete cds	other
34047	2 5041917773	AA194156	ESTs Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (H.sapiens)	other
16929	2 5034481307	AA058952	ESTs	other
26834	2 5028075682	AA287138	ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE (Thermus aquaticus thermophilus)	other
6157	2 5017270258	U80034	Human mitochondrial intermediate peptidase precursor (MIPER) mRNA mitochondrial gene encoding mitochondrial protein complete cds	other
38434	2 5005890672	AA497013	ESTs	?
33269	2 5000262771	W72967	ESTs	other
26991	2 4990009911	AA398284	ESTs	other
7590	2 4948786183	AA173505	ESTs Weakly similar to HYPOTHETICAL 46.1 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION (S.cerevisiae)	other
14960	2 4896232864	UC5237	Human fetal Aiz-60-reactive clone 1 (FAC1) mRNA complete cds	other
13585	2 4866752902	AA455999	ESTs Highly similar to NEUROLYSIN PRECURSOR (Sus scrofa)	other
35901	2 4847873158	AA412151	ESTs	other
38185	2 4826740426	AA487508	Homo sapiens mRNA for KIAA0588 protein complete cds	other
34678	2 4824371274	AA284744	Annexin XI (56kD autoantigen)	other
1424	2 4811113231	J02645	Eukaryotic translation initiation factor 2A	other
16778	2 4800522256	AA047008	ESTs	other
21876	2 4789005203	R43286	EST - RC_R43286	?
17778	2 4685725489	AA149641	ESTs	other
24559	2 4682754649	Z38568	ESTs	other
7781	2 4679471166	AA242904	Homo sapiens proline-rich G1a protein 1 (PRGP1) mRNA complete cds	?
7474	2 4677129013	AA126592	ESTs Weakly similar to No definition line found (C elegans)	other
34290	2 4675270697	AA235866	ESTs	other
5318	2 4673813483	U90905	Human clone 23574 mRNA sequence	TM
10218	2 4645666536	R68884	ESTs Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SCQ2-MRF1 INTERGENIC REGION (Saccharomyces cerevisiae)	other
18109	2 4634292267	AA188981	Homo sapiens retinoblastoma-associated protein HEC mRNA complete cds	?
6485	2 4613518897	X92098	H.sapiens mRNA for transmembrane protein mp24	SS, TM
34964	2 4591845976	AA342959	EST - RC_AA342959	?
42558	2 4588830205	W74751	ESTs	other
27444	2 4585760563	AA430160	ESTs Weakly similar to F25H9.7 (C elegans)	other
21284	2 4582503599	R10301	EST	?
8920	2 4588596729	AF006265	Homo sapiens cancer associated surface antigen (RCAS1) mRNA complete cds	other
30037	2 4544484110	N27439	ESTs	TM
27802	2 4527890177	AA443702	ESTs Weakly similar to WC2B12.7 (C elegans)	TM

FIGURE 8 (cont.)

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3390	2 4525517032	S59184	RYK receptor-like tyrosine kinase	TM
25040	2 452352841	AA010188	ESTs	other
37713	2 4487800271	AA461317	ESTs	other
40477	2 4477660739	N24000	Homo sapiens BAC clone RG300E22 from 7q21-q31.1	other
29382	2 4470532391	H72914	ESTs	other
35521	2 4465885249	AA400831	ESTs	other
20324	2 4464518504	N35406	Phospholipase C beta 4	SS,
19620	2 4460334893	F02506	ESTs	other
21087	2 4406971835	R00186	EST	?
9950	2 4398530157	N71503	ESTs	other
31955	2 4363228422	N93629	ESTs	SS,
15120	2 4345895403	U73524	Human putative ATP/GTP-binding protein (HEAB)	TM
28813	2 4339770686	D58257	mRNA complete cds	other
38062	2 4295434916	AA482284	Human C-1 mRNA complete cds	other
34723	2 428289395	AA287115	ESTs	other
7860	2 427332569	AA285277	Homo sapiens brain expressed ring finger protein mRNA	other
18073	2 4231729031	AA180453	complete cds	other
36755	2 4222443392	AA435698	EST	other
18927	2 4187841215	F11087	EST - RC_AA435698	other
3457	2 4186224787	S74728	ESTs	other
38606	2 4177893475	AA588844	Antiquan	TM
20967	2 41519947	N76086	ESTs	other
24752	2 4141496374	Z40012	ESTs	other
28443	2 4138074256	AA021611	Homo sapiens mRNA for KIAA0587 protein complete	other
452	2 4135942278	D38076	cds	?
11701	2 4134095351	AA253031	ESTs	other
13655	2 412509306	AA458919	RAN binding protein 1	other
24822	2 4118066031	Z40958	Homo sapiens RRM RNA binding protein GRY- (GRY- RBP) mRNA complete cds	other
12672	2 4112720796	AA417067	ESTs Weakly similar to 26S proteasome subunit p4.5 [H. sapiens]	other
4836	2 4106618618	U63717	ESTs	other
47700	2 4083826799	T83729	Human osteocalcin stimulating factor mRNA complete	other
10987	2 4078540866	AA132233	cds	?
35672	2 4073821434	AA404995	EST - RC_T83729	other
6224	2 406310553	X77748	ESTs Highly similar to HYPOTHETICAL 47.4 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]	other
28395	2 404213441	AA610064	EST - RC_AA404895	other
36390	2 4032664297	AA426291	Glutamate receptor metabotropic 3	TM
21045	2 4031905697	N93403	ESTs	other
4558	2 4024665899	U49379	ESTs Weakly similar to No definition line found [C. elegans]	other
12916	2 3996505067	AA427745	ESTs	?
20850	2 3998090334	N69514	Human diacylglycerol kinase epsilon. DGK mRNA	TM
29759	2 3986103066	H99972	complete cds	other
36786	2 3971859161	AA435615	ESTs Weakly similar to oxidoreductase [H. sapiens]	other
31942	2 3947415736	N93185	ESTs	other
7097	2 393322714	AA011452	Human C1b-associated RS cytoplasm CARS-Cyp mRNA	other
39462	2 3938147708	D60063	complete cds	other
14420	2 3919915706	AA600322	ESTs	other
34829	2 3916035475	AA262527	ESTs Highly similar to AAC-RICH MRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]	other
27431	2 3905463084	AA429038	EST - RC_AA262527	other
6387	2 3904071666	X85372	ESTs	TM
11342	2 3902176276	AA223874	H. sapiens mRNA for Sm protein F	other
			Homo sapiens mRNA for KIAA0704 protein partial cds	other

FIGURE 8 (cont.)
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1487	2.358369765	J04068	Telomerase (DNA) II alpha (170kD)	other
9841	2.3641622016	M95724	Centromere autoantigen C	other
11454	2.3820201875	AA233694	ESTs	TM
29950	2.3807499489	N24902	Homo sapiens mRNA for E10-55kDa-associated protein	TM
6398	2.3807187289	AA426176	ESTs Weakly similar to Similar to S cerevisiae hypothetical protein L3111 (H sapiens)	other
32978	2.3805995259	V42768	Human terminal transferase mRNA complete cds	other
27872	2.3784145648	AA459254	ESTs	other
11623	2.3769685069	AA243617	ESTs	other
26582	2.3766857777	AA279768	ESTs	other
22142	2.3761275381	R51382	Homo sapiens mRNA for KIAA0659 protein partial cds	other
13533	2.3758359586	AA454607	ESTs Highly similar to HYPOTHETICAL 402 kD PROTEIN K12H4.3 IN CHROMOSOME II (Caenorhabditis elegans)	other
11534	2.3747649776	AA236223	ESTs	other
5676	2.3709397882	X84229	DEK PROTEIN	other
6231	2.3680994679	X78121	Choroideremia	TM
2382	2.3677644584	M16967	Coagulation factor V	other
22887	2.3673034941	T03314	ESTs	TM
24371	2.3663729415	V487415	ESTs Weakly similar to H1 ALU SUBFAMILY J WARNING ENTRY III (H sapiens)	other
25286	2.3658134948	AA045261	ESTs	other
8054	2.3647542780	G02472	ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR (Homo sapiens)	other
8163	2.3646144577	AA357394	ESTs	other
12233	2.3640777771	AA343513	ESTs Weakly similar to LINE/Ag H-chain fusion protein (M musculus)	SS
22824	2.3634007127	T06195	ESTs	other
14371	2.361524453	AA598219	ESTs Moderately similar to ALR (H sapiens)	other
12401	2.3607293644	AA420229	ESTs	other
26169	2.3599033182	AA251069	ESTs Weakly similar to ORF YOR281c (S. cerevisiae)	?
23095	2.3592943521	T23539	ESTs Highly similar to zinc finger protein (M. musculus)	other
26524	2.3582182239	N53965	ESTs	other
20837	2.3577032218	N69263	ESTs Highly similar to HEXOKINASE TYPE I (Homo sapiens)	other
18201	2.3573132815	AA195358	Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1 the ADORA2BP adenosine A2b receptor LINE pseudogene the IRF6	other
7813	2.3566068562	AA248297	ESTs	TM
21195	2.3547018748	R07210	ESTs	other
13377	2.3513919997	AA449720	Homo sapiens clone 24706 mRNA sequence	other
9714	2.3497245732	L44367	ESTs	other
41537	2.3480892052	R55673	ESTs	other
17352	2.34595172	AA100925	ESTs	other
11914	2.3446613991	AA278907	ESTs	?
24890	2.3440589932	Z41634	ESTs	other
28796	2.3434458024	D51272	EST - RC_D51272_s	?
36796	2.342525534	AA435870	ESTs Weakly similar to B0564.1 (C. elegans)	other
22491	2.3409264581	R70012	EST	other
4788	2.3403776443	U61535	Human calcium-binding protein cDNA complete cds	other
40847	2.3397210986	N86354	ESTs	other
15657	2.3392349306	W63627	Small inducible cytokine A5 (RANTES)	TM
24482	2.3374048148	Z38137	ESTs	other
42022	2.3336939603	T53138	Homo sapiens mRNA for hTCF-4	TM
38233	2.3314720199	AA488023	ESTs	other
41221	2.3310635524	R21531	ESTs Weakly similar to H1 ALU SUBFAMILY J WARNING ENTRY III (H sapiens)	other
8053	2.3297250374	AA309880	ESTs	other

FIGURE 8 (cont.)

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363	2 3275393529	D26528	Human mRNA for RNA helicase complete cds	?
26678	2 3241677974	AA281733	ESTs	other
13407	2 3216524472	AA450200	ESTs	TM
17955	2 3180957399	AA106703	ESTs	TM
31858	2 3160641803	N90680	EST	?
24052	2 3151511584	W42845	Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds	SS
16759	2 3118245547	AA046294	ESTs	other
7861	2 311355404	AA252430	Homo sapiens clone 23797 and 23917 mRNA partial cds	other
41176	2 3111508749	R09379	Natural resistance-associated macrophage protein 2	TM
3860	2 3104335895	U13813	Homolog of Drosophila slowpoke (potassium channel calcium-activated)	TM
40886	2 3077403929	N68149	ESTs Weakly similar to ERV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR (Homo sapiens)	other
19428	2 3068982601	K22949	EST	?
36080	2 3048383557	AA417282	EST - RC_AA417282	other
27264	2 3043527378	AA418389	ESTs	other
13600	2 3031968696	AA456286	ESTs	other
13552	2 3026388376	AA454943	ESTs	other
15664	2 3025773291	W67456	ESTs Moderately similar to YY1-associated factor 2 (H.sapiens)	other
26583	2 3025403178	AA279774	ESTs	?
37434	2 3013886299	AA454149	EST	?
7833	2 2992574443	AA249300	ESTs	other
3674	2 28856113315	U05237	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA complete cds	other
33694	2 284566375	Z38770	ESTs	other
11178	2 2872286082	AA167436	ESTs	?
16977	2 2912855384	AA064616	ESTs	other
19799	2 290119924	H57330	EST	?
6948	2 2900738182	X63337	EST - X63337	?
42097	2 2881548729	T66318	Iso-leucine-tRNA synthetase	?
24247	2 2881065681	V73010	Ribosomal protein L37	other
40879	2 2870463837	N67816	ESTs Moderately similar to III ALU SUBFAMILY SX WARNING ENTRY !!! (H.sapiens)	other
5675	2 2860441014	X59405	Membrane cofactor protein (CD46 trophoblast-lymphocyte cross-reactive antigen)	?
22325	2 2850330577	R60777	ESTs	other
9021	2 2844572929	J05032	ASPARTYL-TRNA SYNTHETASE	other
9239	2 2823045248	D79100	ESTs	other
41897	2 2818672356	T47785	ESTs	other
31105	2 280917152	N63207	EST	?
39565	2 2794194837	F04320	Replication factor C 37-kD subunit	other
7404	2 2793872556	AA094909	Homo sapiens voltage dependent anion channel protein mRNA complete cds	other
6388	2 2788670475	X85373	H.sapiens mRNA for 5m protein G	other
20263	2 2779348551	N31952	ESTs Moderately similar to HYPOTHETICAL 66.5 KD PROTEIN F02A8.5 IN CHROMOSOME III (Caenorhabditis elegans)	other
14529	2 2722894932	AA620307	ESTs	other
21187	2 2718368964	R07320	ESTs	other
28203	2 2692501412	AA490989	ESTs	other
38320	2 2687130032	AA490611	ESTs	other
41625	2 2680307053	R89333	ESTs	other
4674	2 265734645	U54999	Human LGN protein mRNA complete cds	other
26661	2 2637023918	D80037	EST Weakly similar to C50B8.3 (C.elegans)	other
31062	2 2633840539	N82827	ESTs	other
26756	2 2627707292	AA283832	ESTs	other
11567	2 2614480815	AA236747	Homo sapiens mitogen activated protein kinase activated protein kinase gene complete cds	other

FIGURE 8 (cont.)

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25050	2.260506359	AA011134	ESTs Weakly similar to renin [H.sapiens]	TM
41835	2.2593192037	T25681	Human serine kinase mRNA complete cds	other
26895	2.2582387069	AA292765	H.sapiens mRNA for M-phase phosphoprotein mpp5	other
40505	2.2581993488	N34891	Homo sapiens mRNA for KIAA2595 protein partial cds	other
3343	2.2568482074	M97938	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	other
42435	2.2532463427	V46984	ESTs	?
5837	2.2489783488	X62534	High-mobility group (nonhistone chromosomal) protein 2	other
21241	2.2477801609	R09617	ESTs	TM
25756	2.2472585561	AA135868	ESTs	TM
34184	2.2459308213	AA227959	Human cysteine protease Mch2 (isoform alpha (Mch2) mRNA complete cds	other
8672	2.2450884129	AA477048	ESTs	other
7387	2.2447544716	AA093977	ESTs	other
28822	2.2424116577	D59352	ESTs	TM
18016	2.2410305445	AA173223	ESTs	other
20843	2.238288723	N69352	Homo sapiens mRNA for ATP-dependent RNA helicase A46 complete cds	other
10054	2.2387950133	R10266	ESTs Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PHA3-PAC2 INTERGENIC REGION (Saccharomyces cerevisiae)	other
34094	2.2384154308	AA206088	ESTs	other
41246	2.2380827238	R27290	ESTs	other
22634	2.2346537819	R82837	ESTs	other
19688	2.2319351858	H48502	ESTs	SS
34568	2.2306030547	AA280609	ESTs Weakly similar to K0282.3 gene product (C.elegans)	other
28448	2.2295706871	AA621752	Human 26S proteasome-associated pad1 homolog (PDH1) mRNA complete cds	other
20909	2.2284835116	N71704	ESTs	other
651	2.2260763259	D78129	EST - D78129	SS, TM
40409	2.2244318492	H99877	Homo sapiens exportin 1 mRNA complete cds	other
23340	2.224062527	N38825	ESTs	other
23002	2.2233023294	H93005	EST - RC_H93005	other
37321	2.2209252793	AA451898	ESTs	other
8274	2.2208752623	AA402095	ESTs	other
23221	2.2197714612	N28345	ESTs	other
5782	2.2186801223	X54941	CDC28 protein kinase 1	other
4034	2.21808435	U21858	Human transcription initiation factor TFIID subunit TAF831 mRNA complete cds	other
36222	2.2148577598	AA421481	ESTs	other
16567	2.2146935655	AA031591	ESTs	other
4721	2.2134595068	U58046	Human mRNA for KIAA0139 gene complete cds	other
28656	2.2125017907	D19708	Human Gu protein mRNA partial cds	TM
20723	2.2113936194	N66093	ESTs	other
5714	2.2082571749	Y08612	H.sapiens mRNA for Nap68 protein	?
19240	2.205583996	H13265	ESTs	other
36447	2.2050784323	AA426188	ESTs	other
11688	2.202413216	AA252672	Homo sapiens diaphanous biosynthesis protein-2 (DIP-2) mRNA complete cds	other
21650	2.2018153311	R37938	Homo sapiens KIAA0440 mRNA partial cds	other
14152	2.2015953698	AA489780	Homo sapiens Ran-GTP binding protein mRNA partial cds	other
42657	2.1975280207	W62771	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR	other
4642	2.1968027789	U52427	Human RNA polymerase II subunit nrRPS7 mRNA complete cds	?
32779	2.1962611079	W02102	ESTs	TM
38341	2.1951559134	AA490987	ESTs	other
11803	2.1821143838	AA257871	ESTs	other
34835	2.190705129	AA262877	ESTs	TM
39065	2.1895804523	AA620599	ESTs	other

FIGURE 8 (cont.)

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4046	2 1877784122	U22376	MYB PROTO-ONCOGENE PROTEIN	?
11630	2 1876723705	AA242869	ESTs Weakly similar to house-keeping protein (M. musculus)	other
5061	2 1868660566	U78638	Human BRCA1-associated RING domain protein (BARD1) mRNA complete cds	other
33817	2 1804055739	AA157323	ESTs	TM
20674	2 1858972155	NG3392	ESTs	TM
41031	2 1768902734	N91246	ESTs	?
25114	2 1759894688	AA020923	EST	?
24711	2 1768363153	Z39645	ESTs	other
4733	2 1721786534	U58658	Human unknown protein mRNA within the p53 intron 1 complete cds	other
4871	2 1712190791	U66033	Human glypican-5 (GPC5) mRNA complete cds	other
26733	2 1687028853	H99398	EST	?
23155	2 1678113438	T30550	ESTs	other
34638	2 164515923	AA282887	EST	?
35541	2 1621480372	AA000986	Prothymosin alpha	other
1889	2 1598384252	L20591	Anneirin III (lipocortin III)	?
15136	2 1591553983	U68111	PROTEIN PHOSPHATASE INHIBITOR 2	?
40131	2 1583553062	H78779	Homo sapiens histone deacetylase 3 (HDAC3) mRNA complete cds	other
19516	2 156045763	H29207	EST	other
4136	2 1577792237	U26014	ICH-2 PROTEASE PRECURSOR	other
20278	2 1548737104	N32919	ESTs	other
13292	2 1546709291	AA447621	ESTs Highly similar to 40 KD PROTEIN [Borna disease virus]	other
20696	2 154262609	NG3165	ESTs	other
6065	2 1528848242	X88560	Sp3 transcription factor	other
18238	2 1516362853	AA205389	ESTs	other
21627	2 1515099184	R37410	EST	?
3438	2 1502571642	S72024	Eukaryotic translation initiation factor 5A	?
34848	2 1498935434	AA283772	ACTIVATOR 1 35 KD SUBUNIT	other
5964	2 1488964343	X83657	Follicular lymphoma variant translocation 1	SS,
13250	2 1466085975	AA446459	ESTs	other
34370	2 1465845856	AA251829	ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MER2-CPR7 INTERGENIC REGION [Saccharomyces cerevisiae]	other
27996	2 145312871	AA470156	ESTs Weakly similar to dyx11 74K chain cytosolic [R. norvegicus]	SS,
4408	2 13988653247	U41745	Human PDGF associated protein mRNA complete cds	other
4187	2 1395632138	U30888	Human (RNA:guanine transglycosylase) mRNA complete cds	other
10804	2 1366658886	AA093549	ESTs	other
34552	2 1340290702	AA279965	Human mRNA for KIAA0372 gene complete cds	other
18380	2 1331897018	AA227119	ESTs	other
5223	2 1298428563	U83843	EST - U83843	other
37415	2 1270169134	AA453807	EST	other
14582	2 1260941468	AA521340	ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-MUP133 INTERGENIC REGION [Saccharomyces cerevisiae]	other
27756	2 123647107	AA453447	ESTs	other
13787	2 1232868197	AA463745	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]	other
5173	2 1232706565	U81554	Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds	other
40029	2 1214337319	H68221	Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA complete cds	other
19972	2 1193721042	H83639	ESTs	other
23301	2 117519655	T52847	ESTs	other
20504	2 1134521605	N52960	ESTs	other
40145	2 1132200572	H81391	Human mRNA for histamine N-methyltransferase complete cds	other
3461	2 1131164397	S75256	EST - S75256	SS,
41833	2 1124189285	T23611	ESTs	other

FIGURE 8 (cont.)
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39298	2.1092181518	C14805	EST - RC_C14805	other
36021	2.1084568145	AA418876	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521 [H. sapiens]	other
8382	2.1077406838	AA424199	ESTs Weakly similar to C50B8.3 [C. elegans]	other
26288	2.1075583303	AA598447	Homo sapiens exportin 1 mRNA complete cds	other
5807	2.1071008331	X55740	5' nuclease (CD73)	?
19747	2.106109699	H53572	ESTs	other
38155	2.1052335506	AA486777	ESTs	TM
924	2.1037724222	HG1112-HT1112	EST - HG1112-HT1112	?
8544	2.1022261814	H72630	ESTs	other
8384	2.1005713227	AA424282	Human 75-kD autoantigen (PM-Sc1) mRNA complete cds	other
25185	2.1005132894	AA027837	Retinex pigmentosa 3 (X-linked recessive)	SS, TM
24348	2.1000368838	V68469	Tropomyosin alpha chain (skeletal muscle)	?
41401	2.0994868367	R43334	Homo sapiens KIAA0410 mRNA complete cds	other
35340	2.0993782592	AA389900	EST - RC_AA389900	other
10888	2.0990741816	AA112053	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2 (S. cerevisiae)	other
381	2.0974305874	D28473	Isovaleryl-CoA synthetase	other
27051	2.0971755	R49047	ESTs Weakly similar to H1 ALU SUBFAMILY J WARNING ENTRY III (H. sapiens)	other
3293	2.096563118	M94893	Testis specific protein Y-linked	TM
11528	2.0954548212	AA236018	ESTs Weakly similar to unknown (S. cerevisiae)	?
11890	2.0952685865	AA278323	Homo sapiens clone 24608 mRNA sequence	TM
13543	2.0952581265	AA458578	Homo sapiens clone 24477 mRNA sequence	other
15927	2.0952547855	H71829	ESTs	other
36511	2.0927695829	AA429632	ESTs	?
2130	2.0925292202	L40407	Homo sapiens thyroid receptor interactor (TRIP9) gene complete cds	?
7183	2.0924678077	AA046768	Homo sapiens clone TUA8 Cn-du-chat region mRNA	TM
5448	2.0921843187	X02751	Neuroblastoma RAS viral (v-ras) oncogene homolog	?
35956	2.0875765163	AA112533	ESTs	other
7525	2.0870133892	AA149259	ESTs	other
39592	2.0862891765	F09351	ESTs Weakly similar to weakly similar to S. cerevisiae PTM1 precursor [C. elegans]	TM
28029	2.0855738844	AA478476	ESTs	other
18425	2.0855157851	AA232103	ESTs	other
23494	2.0843308062	T70045	ESTs Weakly similar to HYPOTHETICAL 33.2 KD PROTEIN F28A3.7 IN CHROMOSOME 1 [C. elegans]	other
30882	2.0840312831	NS6906	EST	?
32597	2.0839196473	T47333	Human TRIP10 subunit TAF155 (TAF155) mRNA complete cds	other
33368	2.0838178514	W80814	ESTs	other
10259	2.0829121213	R77527	ESTs	other
21882	2.0825457608	R43365	ESTs	other
20590	2.0820571859	NS8146	ESTs	other
12907	2.0807802388	AA427577	ESTs	other
22958	2.0770069487	T10284	ESTs	other
42044	2.0762746251	T58753	ESTs	other
4210	2.0750074179	U31814	Human transcriptional regulator homolog RPD3 mRNA complete cds	other
39	2.074214716	AB003698	Homo sapiens mRNA for Cdc7-related kinase complete cds	other
14350	2.0739236064	AA598831	ESTs	TM
29840	2.0729224128	N71680	ESTs	other
25593	2.0715918096	AA113149	Homo sapiens IPL (IPL) mRNA complete cds	other
26071	2.0708411247	AA236850	Protein phosphatase 2A regulatory subunit B' alpha-1	other
26529	2.0699045563	AA278584	EST	?
12154	2.0692102056	AA291253	ESTs	other
18817	2.0684614007	F10077	ESTs	?

FIGURE 8 (cont.)

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6635	2 0674931973	X93585	H sapiens mRNA for SMT3B protein	other
6681	2 066065203	YD0971	Phosphonobenzyl pyrophosphatase 2	other
22077	2 0647745388	R49482	ESTs	other
11752	2 0645929355	AA256042	ESTs	other
41257	2 0634413834	R31690	ESTs	SS,
6904	2 0622301932	Z34897	Histamine receptor H1	TM
16879	2 060262971	AA056538	ESTs	other
38040	2 0595449295	AA481403	ESTs	other
4111	2 0567536207	U26312	Human heterodysmatin protein HP1Hs-gamma mRNA complete cds	other
32878	2 0546912272	W37448	ESTs	TM
21743	2 0543668448	R40578	ESTs Moderately similar to III ALU SUBFAMILY SX WARNING ENTRY III [H.sapiens]	?
25958	2 0525018401	AA234935	ESTs	other
24659	2 0506511899	Z39211	Homo sapiens GDP-L-fucose pyrophosphorylase (GFPF) mRNA complete cds	other
38030	2 0505994824	AA481148	ESTs	other
61	2 0484705331	AC002115	Cytochrome c oxidase subunit Vlb	?
6306	2 0474040935	X81825	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1	?
6203	2 0473464771	AA382517	EST - AA382517	other
34357	2 0469305727	AA251430	ESTs Highly similar to RAS-RELATED PROTEIN RAB-10 [Caris (amans)]	other
36972	2 0468599712	AA442767	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta polypeptide	other
28156	2 0459278083	AA489057	H sapiens mRNA for nuclear protein SA-2	?
24434	2 045085222	W52787	ESTs	other
33508	2 0449481783	W68772	Human DNA sequence from cosmid F0811 on chromosome 6. Contains Diox BING1 Tapasin RGL2 KEX2 BING4 BING5 ESTs and CpG islands	other
37681	2 04489348104	AA400675	H sapiens mRNA for TRES	other
27125	2 0448698236	AA405505	Homo sapiens mRNA for putative RNA helicase 3' end	other
3780	2 0445300752	U09851	Zinc finger protein 148 (pKZ-52)	other
9112	2 0443252757	D16611	Coproporphyrinogen oxidase (coproporphyrin oxidase)	TM
6357	2 044244223	AA418921	ESTs Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]	other
9133	2 0436113204	D30946	ESTs Highly similar to TRANSLOCATOR-ASSOCIATED PROTEIN GAMMA SUBUNIT [Rattus norvegicus]	TM
7519	2 0414123824	AA147425	EST - AA147425_a	other
14701	2 0413755305	D59324	ESTs	other
380	2 0411495078	D28423	EST - D28423	?
30571	2 0348528804	N49595	ESTs	other
825	2 0329522889	D87328	Holocarboxylase synthetase (biotin-(propionyl)-Coenzyme A-carboxylase (ATP-hydrolyzing)) ligase	TM
27744	2 0318041265	AA452818	ESTs Weakly similar to HYPOTHETICAL PROTEIN H10034 [Haemophilus influenzae]	other
3997	2 0311206335	U19906	Arginine vasopressin receptor 1 (AVPR1)	?
22717	2 0302732387	R91394	EST - RC_R91394	?
377	2 0289078264	D28364	EST - D28364	other
28581	2 0274006652	C21163	EST	other
11790	2 0269672127	AA256678	ESTs Highly similar to POP3 PROTEIN [Saccharomyces cerevisiae]	other
37931	2 0269058272	AA478523	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	other
24678	2 0206818539	Z39349	ESTs Weakly similar to VACUOLAR ATP SYNTHASE 54 KD SUBUNIT [Saccharomyces cerevisiae]	other
10940	2 0209035614	AA122217	ESTs Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III [C.elegans]	other
13964	2 0207518872	AA479048	ESTs	?
15665	2 019773566	W67631	Homo sapiens clone 24538 mRNA sequence	TM
28379	2 0183373185	AA609710	ESTs	other
13349	2 0172119305	AA449269	ESTs Weakly similar to MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR [Neurospora crassa]	SS,
7322	2 0167797945	AA090692	ESTs Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]	other
29358	2 0165298752	H70641	EST - RC_H70641	?

FIGURE 8 (cont.)

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24230	2 016017662	W72276	ESTs	other
40212	2 0150778189	H88535	Human clone 121711 defective manner transposon Heme2 mRNA sequence	?
729	2 01573779	D83778	Human mRNA for KIAA0194 gene partial cds	other
17851	2 0144787235	AA165526	Homo sapiens bifunctional ATP sulfurylase/adenosine 5-phosphosulfate kinase mRNA complete cds	other
33943	2 0135709277	AA171739	ESTs	other
5870	2 0118426199	X59244	Zinc finger protein 43 (MTF6)	other
36319	2 0118529739	AA425107	ESTs	other
75654	2 0097423819	AA126851	ESTs Weakly similar to DNA-directed RNA polymerase (D melanogaster)	other
16344	2 0090457727	AA018907	ESTs	?
8118	2 0090099575	AA320593	ESTs	other
29962	2 0087628088	N25228	ESTs	TM
32236	2 0078250756	R49327	Natural resistance-associated macrophage protein 2	TM
3279	2 0072427596	M94065	DIHYDROOROTATE DEHYDROGENASE PRECURSOR	TM
16255	2 0065069683	AA013349	ESTs	other
37872	2 0059275226	AA478215	EST - RC_AA478215	TM
41256	2 005856844	R31577	ESTs	other
34834	2 0050133743	AA282655	ESTs	other
23168	2 0038279023	T33215	ESTs	other
29851	2 0034762985	N22145	ESTs	other
32862	2	VQ2519	EST	?

FIGURE 8 (cont.)

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New Key Number	Accession	fold upregulated of Tumor over normal colon	Unigene Descriptor	
104660	AA007160	23	ESTs	SS
130016	AA055811	14	transmembrane glycoprotein	SS, TM
104954	AA074514	10	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]	Other
105082	AA143763	7	ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C.elegans]	Other
109141	AA176428	7	ESTs	Other
108893	AA135894	6	retinoic acid induced 3	TM
108927	AA143493	5	ESTs; Weakly similar to PLECKSTRIN [H.sapiens]	Other
109027	AA157818	5	Human endogenous retroviral protease mRNA; complete cds	Other
133015	AA047036	4	ESTs	Other
114545	AA056263	4	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Other
104974	AA085918	4	H.sapiens HUNK1 mRNA	Other
108695	AA121315	4	ESTs	SS
105049	AA132554	4	ESTs; Moderately similar to myosin heavy chain 12 [H.sapiens]	Other
133834	AA147510	4	Homo sapiens serine protease mRNA; complete cds	Other
109244	AA194237	4	ESTs; Weakly similar to C17H11.6 [C.elegans]	Other
128411	AA007555	3	ESTs; Weakly similar to transformation-related protein [H.sapiens]	SS, TM
114509	AA043551	3	ESTs	Other
104688	AA053680	3	ESTs	Other
114542	AA055768	3	ESTs	SS
132718	AA056731	3	Sjogren syndrome antigen A2 (60kD; ribonucleoprotein autoantigen SS-A/Ro)	Other
104953	AA074157	3	ESTs	Other
132784	AA089589	3	GDP dissociation inhibitor 2	Other
130962	AA102051	3	transmembrane 4 superfamily member 6	SS, TM
134421	AA122386	3	collagen; type V; alpha 2	SS
105035	AA126486	3	ESTs	Other
105039	AA130349	3	ESTs	Other
105062	AA134968	3	ESTs	Other
133617	AA148318	3	Human mRNA for KIAA0069 gene; partial cds	TM

FIGURE 9

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		ESTs: Highly similar to CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN	
130335	AA156499	3: [H.sapiens]	Other
105132	AA159501	3: HBV associated factor	Other
109042	AA159525	3: ESTs	Other
109043	AA159605	3: ESTs	Other
132669	AA188378	ESTs: Weakly similar to 60S RIBOSOMAL 3: PROTEIN L22 [H.sapiens]	Other
135398	AA194075	3: nuclear receptor coactivator 4	Other
109344	AA213696	3: ESTs	SS
133221	AA235289	ESTs: Highly similar to rap2 gene product 3: [H.sapiens]	Other
114496	AA035611	ESTs: Weakly similar to IIII ALU SUBFAMILY SX WARNING ENTRY !!!! 2: [H.sapiens]	Other
128635	AA043959	2: tropomyosin 4	Other
129912	AA047344	ESTs: Weakly similar to similar to WW/rsp5/WWP domain containing proteins 2: [C.elegans]	Other
104927	AA058855	2: ESTs	SS
132821	AA070724	CD44 antigen (homing function and Indian 2: blood group system)	Other
108409	AA075578	zm88h3.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 2: IMAGE:54545 3', mRNA sequence"	Other
133621	AA076138	2: H2A histone family; member Y	Other
108565	AA085342	ATPase; Ca++ transporting; cardiac 2: muscle; slow twitch 2	TM
104977	AA088228	2: ESTs	Other
103777	AA093131	Homo sapiens PAC clone DJ0157F23 from 2: 7p15	Other
108649	AA112540	2: ESTs	Other
114692	AA121998	ESTs: Weakly similar to Similar to 2: potassium channel protein. [C.elegans]	Other
105063	AA134985	2: ESTs	Other
133273	AA147725	2: dendritic cell protein	Other
128515	AA149044	ESTs: Highly similar to the KIAA0195 gene 2: is expressed ubiquitously. [H.sapiens]	SS
105182	AA191014	ESTs: Weakly similar to Ydr372cp 2: [S.cerevisiae]	Other
109277	AA196332	2: ESTs	Other
132608	AA199588	ARP3 (actin-related protein 3; yeast) 2: homolog	Other
109380	AA219015	2: ESTs	Other
130800	AA223385	ESTs: Weakly similar to katanin p80 2: subunit [H.sapiens]	Other
129945	AA232104	ESTs: Highly similar to (define not 2: available 4929579) [H.sapiens]	Other
105305	AA233609	2: spindle pole body protein	Other

FIGURE 9

(Cont.)

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128924	AA234962	2. ESTs	TM
114895	AA236177	Homo sapiens mRNA for KIAA0887 protein; 2' partial cds	Other

FIGURE 9 (Cont.)

FIGURE 10
1 of 8

A	B	C	D	E
1	Human alpha satellite and satellite 3 junction DNA sequence	AA11502	Human alpha satellite and satellite 3 junction DNA sequence	7
2	ESTs; Weakly similar to serine protease [H sapiens]	D13666	ESTs; Weakly similar to serine protease [H sapiens]	7
3	27090	AA11502	Human alpha satellite and satellite 3 junction DNA sequence	7
4	232	D13666	ESTs; Weakly similar to serine protease [H sapiens]	7
5	25481	AA102520	ESTs; Weakly similar to heat shock protein hsp90 homolog [H sapiens]	SS
6	27685	AA453783	ESTs; Weakly similar to heat shock protein hsp90 homolog [H sapiens]	TM
7	39492	F13673	ESTs	other
8	28050	AA489037	H sapiens mRNA for nuclear protein SA-2	7
9	31485	N11781	ESTs	other
10	25606	AA132514	densely-regulated protein	other
11	7600	Z14816	collagen, type I, alpha 2	SS
12	25931	AA236200	ESTs	other
13	12118	AA291528	ESTs	other
14	32813	W46810	HMT1 (hHR23 methyltransferase; S. cerevisiae) like 2	other
15	26864	AA393604	H beta 58 homolog	other
16	22514	R78392	ESTs	other
17	25466	AA112019	lactate dehydrogenase A	TM
18	32276	R92994	matrix metalloproteinase 12 (macrophage elastase)	SS
19	32485	T32108	ESTs	other
20	22430	R71082	TFAR19 novel apoptosis-related gene	other
21	30052	N32586	ESTs; Weakly similar to Ydr33cp [S. cerevisiae]	other
22	28354	C14037	ESTs; Weakly similar to Ydr33cp [S. cerevisiae]	?
23	29604	H08555	Homo sapiens gene for NBS1, complete cds	TM
24	27592	AA449417	Homo sapiens mRNA for putative glucosyltransferase, partial cds	TM
25	28691	D51276	STATHMIN	other
26	19100	H10933	ESTs	other
27	5891	X60486	H4 histone family, member G	7
28	12285	AA394243	ESTs; Highly similar to RSPs protein [Saccharomyces cerevisiae]	other
29	23629	T85700	ESTs	other
30	23951	AA236672	ESTs; Weakly similar to DFS7 [H. sapiens]	other
31	477	D38593	Human mRNA for calguzarin, complete cds	?
32	11153	AA188897	ESTs	TM
33	27183	AA421562	Homo sapiens secreted cement gland protein XAG-2 homolog (XAG-2R)	SS
34	32899	W45728	ESTs; Highly similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN	other
35	9576	J03464	collagen, type I, alpha 2	SS
36	10506	AA027089	ESTs; Highly similar to HYPOTHETICAL 1.4 KD PROTEIN IN UBP4-SPT	other
37	22084	R51309	ESTs	other
38	39217	C21242	calpain 2	other
39	2813	M20540	CARCINOEMBRYONIC ANTIGEN PRECURSOR	TM
40	27553	AA440965	ESTs	TM
41	40031	H33442	calichest-O-methyltransferase	other
42	10131	R55153	polyubiquitin initiation factor 2, subunit 8 (48kD)	other
43	23154	AA043353	ESTs; Highly similar to UBQUITIN-CONJUGATING ENZYME E2-17 KD	other
44	25821	AA164843	ESTs; Weakly similar to Ks-167 intracellular antigen [H sapiens]	other

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FIGURE 10 (CONT)
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A	B	C	D	E
45	2604	A243297	ESTs: Weakly similar to PEANUT PROTEIN [Drosophila melanogaster]	other
46	27055	A406942	ESTs	other
47	10044	A4100710	non-specific cross reacting antigen	other
48	11358	A4332104	ESTs	other
49	17389	A4121315	ESTs	other
50	17415	A4122389	Collagen, type V, alpha 2	?
51	23772	B82735	ESTs	TM
52	25531	A4070947	tropomyosin 4	other
53	25359	A4070138	histone macroH2A1.2	other
54	27039	A406145	ESTs	SS, TM
55	27261	A425544	Homo sapiens clone 23693 mRNA, complete cds	other
56	28785	D80946	SFRS protein kinase 1	other
57	32192	R67275	collagen, type XI, alpha 1	other
58	3003	M77349	transforming growth factor, beta-induced; 6kD	other
59	5519	X06700	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal co	SS
60	5582	X12576	keratin 15	other
61	11618	A4251902	Homo sapiens lysophospholipase (LPL) mRNA, complete cds	other
62	17606	A4147725	Homo sapiens GA17 protein mRNA, complete cds	other
63	18024	A4188378	ESTs: Highly similar to CS RIBOSOMAL PROTEIN L22 [Rattus norvegicus]	other
64	20941	N90993	ESTs	other
65	13612	A4456889	ESTs: Highly similar to (define not available 412715) [H. sapiens]	TM
66	17789	A4157818	Human endogenous retroviral protease mRNA, complete cds	other
67	25344	A4075182	Sjogren syndrome antigen A2 (8kD; ribonucleoprotein autoantigen SS-A/R	?
68	25583	A4131182	ESTs	other
69	32170	R61297	eukaryotic translation initiation factor 3; subunit 6 (48kD)	other
70	33586	M18728	cytoplasmic protein complex; subunit alpha	SS
71	2396	Z36595	non-specific cross reacting antigen	other
72	3251	M93036	membrane component; chromosomal 4; surface marker (35kD glycoprotein)	other
73	8158	A437830	Homo sapiens GW112 protein (GW112) mRNA, complete cds	other
74	9207	D78032	ESTs: Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 GAMM	other
75	15951	U64661	Human poly(A)-binding protein processed pseudogene3	?
76	15914	W63827	ESTs: Moderately similar to IIII ALU SUBFAMILY SP WARNING ENTRY II	TM
77	25323	A4070485	Homo sapiens clone 23967 unknown mRNA; partial cds	other
78	25329	A4070827	ESTs: Weakly similar to KIAA18 [H. sapiens]	TM
79	25549	A4127058	ESTs: Weakly similar to predicted using GeneFinder [C. elegans]	TM
80	25584	A4131185	telomeric nuclear ribonucleoprotein A2/B1	other
81	27468	A441971	Homo sapiens mRNA for KIAA494 protein, complete cds	TM
82	32012	R31180	ESTs	?
83	30087	A4408951	Homo sapiens chaperonin containing 1-complex polypeptide 1; beta subunit	other
84	38457	A4598714	Lon protease-like protein	other
85	39421	F03974	H. sapiens mRNA for Sop2p-like protein	other
86	3758	U09587	glycyl-tRNA synthetase	other
87	8952	C00038	ESTs	TM
88	12576	A431191	ESTs	other

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FIGURE 10 (CONT)
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	A	B	C	D	E
89	17827	2.8	AA135604	Homo sapiens putative G protein-coupled receptor (RAIG1). Retinoid acid II	TM
90	20752	2.8	N6921	ESTs; Weakly similar to neopterin [H.sapiens]	other
91	22954	2.6	T17185	ESTs	TM
92	25808	2.6	AA161161	ESTs	other
93	27169	2.6	AA410878	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	other
94	28086	2.6	AA480882	ESTs; Moderately similar to ubiquitin TPR motif, Y isoform [H.sapiens]	other
95	28705	2.8	D54289	ESTs	other
96	33593	2.6	Z39041	ESTs; Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGE	TM
97	37383	2.8	AA455521	E2F transcription factor 5; p13-binding	other
98	39170	2.8	C15324	ESTs	SS, TM
99	39251	2.5	D20002	HLMG5972 Human promyelocytic Homo sapiens cDNA clone pm2344.3	other
100	2767	2.5	N37583	H2A histone family, member Z	other
101	5468	2.5	X04347	heterogeneous nuclear ribonucleoprotein A1	other
102	9243	2.5	D82406	Homo sapiens mRNA for 5-aminimidazole-4-carboxamide-1-beta-D-ribose	other
103	14791	2.5	T35725	ESTs; Highly similar to HYPOPHOSPHATE 4.2 KO PROTEIN IN SCOT-MR	other
104	14804	2.5	T48195	eukaryotic translation initiation factor 3, subunit 3 (gamma; 4KD)	other
105	16974	2.5	AA070724	CD44 antigen (homolog function and Indian blood group system)	other
106	20031	2.5	N21085	Homo sapiens androgen receptor associated protein 24 (ARQ24) mRNA; c	?
107	25484	2.5	AA112679	ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sapiens]	TM
108	26330	2.5	AA347359	lysosyme (renal amyloidosis)	SS
109	26668	2.5	AA490212	histone macroH2A1.2	other
110	30071	2.5	N33011	replication protein A3 (14KD)	other
111	32740	2.5	V01800	von Hippel-Lindau syndrome	other
112	35870	2.5	AA416785	heterogeneous nuclear ribonucleoprotein A1	other
113	41908	2.5	T59161	Thymosin beta 1	TM
114	60111	2.4	X66401	proteasome (prosome, macropain) subunit, beta type, 8 (large multi-function)	?
115	9201	2.4	D63079	ESTs; Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAI	other
116	9218	2.4	D78891	ESTs	TM
117	10065	2.4	R32993	ESTs; Highly similar to LEUCYL- RNA SYNTHETASE; CYTOPLASMIC [other
118	10253	2.4	R22411	DEK gene	other
119	11107	2.4	R22411	ESTs; Moderately similar to RBCP2 [H.humans]	other
120	11846	2.4	AA155501	ESTs; Weakly similar to similar to Yeast hypothetical protein L6167, 12 like	other
121	12767	2.4	AA262969	ESTs; Weakly similar to uroporphyrinogen III synthase; UROIII [H.sapiens]	SS
122	13772	2.4	AA424348	ESTs; Weakly similar to alternative spliced product using exon 13A [H.sapiens]	other
123	16728	2.4	AA464703	cadherin 17, LI cadherin (liver-liver-liver)	SS, TM
124	17174	2.4	AA053102	ESTs; Highly similar to (define not available 412715) [H.sapiens]	other
125	21366	2.4	AA158243	ESTs	other
126	23433	2.4	R24059	GDP dissociation inhibitor 2	TM
127	25603	2.4	AA095969	Homo sapiens CAGH1a (CAGH1) mRNA, partial cds	other
128	25791	2.4	AA132032	ELK1, modif kinase	other
129	28153	2.4	AA252827	ESTs	?
130	26852	2.4	AA385527	ESTs; Weakly similar to T1.5-associated protein T1.5R [H.sapiens]	other
131	27122	2.4	AA416877	ESTs	other
132	28385	2.4	C14090	actin, gamma 1	other

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FIGURE 10 (CONT)
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	A	B	C	D	E
133	26526	2.4	D25560	Homo sapiens DNA from chromosome 19-coamid H2619 containing USF2;	other
134	26667	2.4	D51241	Homo sapiens mRNA for putative vacuolar protein ATPase membrane sec	SS, TM
135	26850	2.4	N24968	vacuolar H(+)-ATPase subunit	other
136	32892	2.4	W44457	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	other
137	33811	2.4	AA173143	heterogeneous nuclear ribonucleoprotein G	other
138	40121	2.4	I93492	ESTs; Highly similar to villin [H.sapiens]	other
139	40141	2.4	H94877	ESTs; Moderately similar to putative G-binding protein [H.sapiens]	other
140	40167	2.4	H95237	collagen, type XI, alpha 1	other
141	446	2.3	D38073	minichromosome maintenance deficient (S. cerevisiae) 3	other
142	3530	2.3	S81914	DIFFERENTIATION-DEPENDENT GENE 2	other
143	7835	2.3	AQ32438	Homo sapiens tyrophosphatase (LPL) mRNA, complete cds	other
144	10898	2.3	AA121879	proteasome (prosome; macropain) subunit, beta type; 9 (large multifunction	other
145	10955	2.3	AA134138	ESTs; Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]	other
146	11015	2.3	AA143763	ESTs; Weakly similar to similarity to S. Pombe BEM1/BUD3 suppressor [C	other
147	11895	2.3	AA278420	ESTs; Highly similar to [define not available 433735] [H.sapiens]	TM
148	13398	2.3	AA451676	ESTs	other
149	15484	2.3	V20391	proliferation-associated 284; 36kD	other
150	17619	2.3	AA135406	ESTs	other
151	18225	2.3	AA213686	ESTs	other
152	20450	2.3	N53927	ESTs; Weakly similar to phenylalanylamine binding protein [H.sapiens]	7
153	25308	2.3	AA065227	ESTs; Weakly similar to coded for by C. elegans cDNA Y1C1.3 [C. elegans]	other
154	26590	2.3	AQ321151	ESTs; Weakly similar to predicted using GeneIndex [C. elegans]	other
155	27624	2.3	AA452112	Homo sapiens mRNA for putative theonodrin-like protein	other
156	27792	2.3	AA460359	ESTs; Weakly similar to DNA-DIRECTED RNA POLYMERASE II 14 KD P	7
157	28231	2.3	AA600153	DEK gene	other
158	28722	2.3	D59711	ESTs	other
159	30383	2.3	N47958	eukaryotic translation initiation factor 3, subunit 3 (gamma; 4kD)	other
160	32928	2.3	W47820	ESTs; Weakly similar to reverse transcriptase related protein [H.sapiens]	other
161	39585	2.3	H11320	Homo sapiens FRHFPB2115 mRNA; partial cds	TM
162	40175	2.3	H86655	peptidylprolyl isomerase B (cyclophilin B)	other
163	40366	2.3	N26891	ESTs; Highly similar to [define not available 467914] [H.sapiens]	other
164	40733	2.3	N67422	ESTs; Weakly similar to 25 kDa trypsin inhibitor [H.sapiens]	other
165	4918	2.2	U88105	poly(A)-binding protein-like 1	7
166	5165	2.2	U81607	GRAVIN	other
167	12242	2.2	AQ372018	ESTs	other
168	13154	2.2	AA442768	Homo sapiens inner mitochondrial membrane translocase Tim23 (TIM23)	7
169	14276	2.2	AA559450	ESTs	other
170	15721	2.2	W95348	ESTs	other
171	20588	2.2	N62945	Homo sapiens hMm17A1b mRNA, complete cds	TM
172	24021	2.2	W42857	ESTs	TM
173	24250	2.2	V984712	calumenin	other
174	25245	2.2	AQ033768	ESTs	SS
175	25430	2.2	AA099429	SPlicing FACTOR U2AF 35 KD SUBUNIT	TM
176	25562	2.2	AA178904	heterogeneous nuclear ribonucleoprotein U (scalloid attachment factor A)	other

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FIGURE 10 (CONT)

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	A	B	C	D	E
177	26745	2.2	D60465	caldesmon 1	other
178	31097	2.2	R20669	tumor rejection antigen (gp96) 1	other
179	32481	2.2	T47333	Human TFIID subunit TAF155 (TAF155) mRNA, complete cds	other
180	35636	2.2	T93807	high-mobility group (nucleosome chromosomal) protein 1	other
181	37703	2.2	AA170237	ESTs; Weakly similar to uroporphyrinogen III synthase, UROIIIH [H.sapien]	TM
182	215	2.1	D13627	Human mRNA for KIAA2 gene, complete cds	TM
183	2449	2.1	M21259	small nuclear ribonucleoprotein polypeptide E	?
184	3205	2.1	M68458	ER LUMEN PROTEIN RETAINING RECEPTOR 2	TM
185	4197	2.1	U31556	E2F transcription factor 5; p13-binding	other
186	4811	2.1	U62862	eukaryotic translation initiation factor 3; subunit 6 (48kD)	other
187	5417	2.1	X01060	transferrin receptor (p57 CD71)	TM
188	6334	2.1	X63228	cadherin 17; L1 cadherin (liver-ectoderm)	SS, TM
189	6605	2.1	X58133	NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR	?
190	10471	2.1	AA024492	ESTs; Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sa]	other
191	11027	2.1	AA140318	Human mRNA for KIAA099 gene, partial cds	TM
192	11116	2.1	AA161292	INTERFERON-ALPHA INDUCED 11.3 KD PROTEIN	other
193	11540	2.1	AA238972	ESTs; Moderately similar to III ALU SUBFAMILY J WARNING ENTRY IIII	other
194	11937	2.1	AA280865	ESTs; Weakly similar to Similarity to Yeast hypothetical protein YOR3180	other
195	17312	2.1	AA111889	pigment epithelium-derived factor	other
196	18286	2.1	H18947	ESTs	other
197	20122	2.1	N26259	ESTs; Weakly similar to uroporphyrinogen III synthase, UROIIIH [H.sapien]	other
198	20948	2.1	N91492	Homo sapiens clone 628 unknown mRNA, complete sequence	other
199	20997	2.1	N98464	ESTs	other
200	27106	2.1	AA172432	ESTs	other
201	28036	2.1	AA488433	ESTs; Weakly similar to deduced amino acid sequence is highly homologous	other
202	28187	2.1	AA521256	ESTs; Highly similar to nuclear pore complex protein NUP17 [R.nonvegus]	other
203	28336	2.1	AA621604	ESTs	other
204	28719	2.1	D59370	ESTs	other
205	28886	2.1	F04674	Homo sapiens mRNA for KIAA218 protein, partial cds	other
206	32124	2.1	R46608	eukaryotic translation initiation factor 3; subunit 7 (26kD, 66kD)	other
207	33433	2.1	W80444	ESTs; Highly similar to (define not available, 4454524) [H.sapien]	other
208	33564	2.1	W96151	ESTs; Moderately similar to ganglioside-induced differentiation associated	?
209	35778	2.1	AA172770	ESTs	other
210	35868	2.1	AA608751	calhesin B	other
211	39301	2.1	D57317	Human transcriptional corepressor PC4 mRNA, complete cds	SS
212	39945	2.1	H73484	ESTs; Weakly similar to similar to Yeast hypothetical protein LB187.12 box	SS, TM
213	39977	2.1	H78323	Homo sapiens E2F-related transcription factor (DP-1) mRNA, complete cds	other
214	40378	2.1	N27188	ESTs	other
215	41765	2.1	T28789	ESTs; Highly similar to TYROSINE-PROTEIN KINASE RECEPTOR EPH-	TM
216	1714	2	LC9604	proteoglycan protein 2 (ectopic epithelium-enriched)	TM
217	2001	2	L33930	Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region	TM
218	3278	2	M94358	single-stranded DNA-binding protein	other
219	4145	2	U28749	high-mobility group (nucleosome chromosomal) protein isoform LC	TM
220	6149	2	AA354267	ESTs; Highly similar to HYPOTHETICAL 58.7 KD PROTEIN ZK757.1 IN C	other

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FIGURE 10 (CONT)
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	A	B	C	D	E
221	9844	2	N33807	ESTs: Highly similar to NEDD-4 PROTEIN [Homo sapiens]	other
222	14032	2	AA46002	ESTs: Weakly similar to CH-TOG PROTEIN [H. sapiens]	TM
223	15395	2	AA025873	ESTs: Moderately similar to (define not available 416878) [H. sapiens]	TM
224	17327	2	AA112540	ESTs	TM
225	23003	2	T30081	ubiquitin-conjugating enzyme E2E 1 (homologous to yeast UBC4/5)	other
226	25625	2	AA133569	ESTs: Weakly similar to neuronal thread protein AD7c-MTP [H. sapiens]	other
227	28073	2	AA490094	ESTs	other
228	28700	2	D51139	ribosomal protein S28	other
229	29055	2	H27188	collagen-binding protein 2 (colligen 2)	other
230	32191	2	R67083	cathepsin	SS, TM
231	32887	2	W45664	5' nucleotidase (CD73)	other
232	10782	1.6	AA074880	ESTs: Weakly similar to HYPOTHETICAL 95, KO PROTEIN IN CPA3A1P	other
233	21785	1.6	AA460454	ESTs: Weakly similar to KIAA512 protein [H. sapiens]	other
234	26706	1.6	D94286	Human mRNA for KIAA3255 gene; complete cds	TM
235	36414	1.6	AA430166	ESTs	other
236	9979	1.5	N91087	ESTs: Weakly similar to F55A12.9 [C. elegans]	TM
237	9937	1.5	N95507	ESTs: Weakly similar to KIAA318 [H. sapiens]	other
238	10656	1.5	AA047280	ESTs	other
239	14877	1.5	U37546	apoptosis inhibitor 1	TM
240	27065	1.5	AA10264	Human mRNA for KIAA339 gene; complete cds	other
241	29278	1.5	H72948	huglycan	SS
242	31917	1.5	N98238	ESTs	other
243	36272	1.5	AA495533	ESTs	other
244	41396	1.5	R55342	CO68 antigen	other
245	41958	1.5	T87710	ESTs	?
246	8439	1.4	AA439304	Homo sapiens androgen receptor associated protein 24 (ARAZ4) mRNA; c	other
247	10311	1.4	AA001936	ESTs	other
248	16559	1.4	AA112149	ESTs	other
249	11278	1.4	AA213410	ESTs	SS
250	13548	1.4	AA456033	ESTs: Highly similar to HYPOTHETICAL 1,4 KO PROTEIN IN UBPS-SPT	other
251	14340	1.4	AA599553	Homo sapiens TCFL5 mRNA for transcription factor-like 5; complete cds	other
252	32180	1.4	R63777	ESTs	other
253	35187	1.4	AA398722	ESTs	other
254	37254	1.4	AA453483	ESTs	TM
255	1344	1.3	HG4757-HT5207	"Oncogene MIA-4", Fusion Activated"	other
256	5397	1.3	V01516	KERATIN, TYPE II CYTOSKELETAL 6D	SS, TM
257	16272	1.3	AA018922	core promoter element binding protein	other
258	23427	1.3	T76358	ESTs: Highly similar to POL POLYPROTEIN [Simian sarcoma virus]	other
259	25718	1.3	AA150741	gene with multiple splice variants near HD locus on 4p16.3	other
260	33459	1.3	V93403	ESTs	other
261	36574	1.3	AA34454	ESTs: Weakly similar to or: hypothetical protein [E. coli]	SS
262	41546	1.3	R82846	insulin-like growth factor 2 (somatomedin A)	other
263	2368	1.2	M17653	insulin-like growth factor 2 (somatomedin A)	TM
264	6388	1.2	X66371	lethal giant larvae (Drosophila) homolog 1	other

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FIGURE 10 (CONT)
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A	B	C	D	E
265	24427	23208	ESTs	other
266	27089	AA411473	adducin 1 (alpha)	other
267	33177	WT3195	ESTs	other
268	34852	AA347891	ESTs	?
269	35325	AA400270	ESTs	other
270	36609	AA435668	ESTs; Weakly similar to putative p15 [H sapiens]	other
271	38477	AA398939	ESTs	other
272	40975	R02547	ESTs	other
273	41874	TS1150	ESTs	other
274	8235	AA401047	Homo sapiens mRNA for neuropilin; complete cds	other
275	9772	ML1349	SERUM AMYLOID A-4 PROTEIN PRECURSOR	SS
276	14758	S83188	BPLP	other
277	15831	X30579	H sapiens DNA for cyp related pseudogene	?
278	20656	N6289	ESTs	other
279	24881	AA004502	cerebroside (3'-phosphoadenylyl sulfate galactosylceramide 3') sulfotransferase	TM
280	25045	H13549	ESTs	other
281	31584	N74690	ESTs	TM
282	31840	N73784	Homo sapiens Bin1EL mRNA; complete cds	other
283	35293	AA400013	EST	other
284	37583	AA481489	ESTs	other
285	37852	AA479896	ESTs	other
286	38397	AA521342	ESTs	other
287	38552	AA609018	ESTs	other
288	40397	N29883	ESTs; Moderately similar to III ALU CLASS C WARNING ENTRY III [H sa]	other
289	40488	N40559	ESTs; Highly similar to LEUKOTOXIN SECRETION ATP-BINDING PROT	other
290	41231	R41772	EST	other
291	41333	R48580	ESTs	other
292	3255	M83143	"Homo sapiens plasminogen-like protein (PLGL) mRNA, complete cds"	other
293	5742	X53065	Accretion not listed in Genbank	?
294	6007	X66383	SERINE/THREONINE-PROTEIN KINASE PC1AIRE-1	other
295	15233	W04960	ESTs	other
296	15262	WT7304	Homo sapiens mRNA for KMA97 protein; complete cds	other
297	15383	W26847	ESTs; Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MS	other
298	15608	W58725	mitogen-activated protein kinase-activated protein kinase 2	TM
299	18435	AA233898	ESTs	other
300	21738	R41998	ESTs	other
301	23508	AA058881	Tm13a.1.1 Stratiopene paraceras (p93728) Homo sapiens cDNA clone INA	TM
302	28111	H04088	ESTs; Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H sa]	other
303	34743	AA302772	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H sapiens]	other
304	34601	AA342528	ESTs; Moderately similar to unknown [H sapiens]	other
305	35355	AA400521	ESTs	other
306	38940	AA446449	ESTs	other
307	39221	C21330	ESTs	other
308	1322	HG4535-IT4940	Domain	other

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FIGURE 10 (CONT)
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	A	B	C	D	E
309	9842	0.9	NR4146	ESTs	other
310	10084	0.9	R32822	ESTs	other
311	11701	0.9	AA255546	ESTs	other
312	12088	0.9	AA287568	Human mRNA for KIAA107 gene, complete cds	other
313	15287	0.9	W19098	ESTs	other
314	15901	0.9	Z20005	immunoglobulin superfamily, member 3	SS
315	21906	0.9	R45512	ESTs	other
316	22002	0.9	R49459	ESTs	other
317	23136	0.9	T40327	ESTs	other
318	26673	0.9	D43719	ESTs	other
319	29159	0.9	H60824	ESTs	other
320	32610	0.9	T69122	Human clone 23732 mRNA, partial cds	SS TM
321	32674	0.9	W02129	EST	other
322	35428	0.9	AA401409	ESTs	other
323	38504	0.9	AA392209	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H sapiens]	other
324	244	0.8	D14446	fibrinogen-like 1	TM
325	14204	0.8	AA496980	ESTs	other
326	25260	0.8	AA056210	ESTs	other
327	6971	0.7	N67590	ESTs	other
328	20461	0.7	N54429	ESTs	other
329	41029	0.7	R06816	Homogentisate 1,2-dioxygenase (homogentisate oxidase)	other
330	41985	0.6	T11012	fibrinogen, B beta polypeptide	SS TM

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FIGURE 11
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
134804	12.3	L37036	small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)	TM
130617	11.4	M90516	glutamine-fructose-6-phosphate transaminase 1	TM
104209	10.6	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated	SS
109991	10	H09813	ESTs	TM
124315	8.3	H94892	v-rat simian leukemia viral oncogene homolog A (ras related)	Other
132977	8.2	U28686	RNA binding motif protein 3	Other
130407	7.4	N29888	ESTs	Other
116176	6.6	AA463725	ESTs; Weakly similar to KIAA0226 [H.sapiens]	Other
119271	6.5	T16387	ESTs	Other
134711	6.5	X04011	cytochrome b-245; beta polypeptide (chronic granulomatous disease)	TM
134326	6.1	U16306	"Human chondroitin sulfate proteoglycan versican V splice-variant precursor peptide mRNA, complete cds"	Other
125852	5.9	H09290	ESTs; Weakly similar to unknown [H.sapiens]	SS, TM
112109	5.9	R48589	ESTs	TM
132528	5.9	AA283008	chromosome-associated polypeptide C	Other
134367	5.7	X54199	phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide synthetase; phosphoribosylaminoimidazole synthetase	Other
111829	5.2	R40057	prominin (mouse)-like 1	SS, TM
102165	5	U18321	Death associated protein 3	Other
130441	5	U35835	protein kinase; DNA-activated; catalytic polypeptide	Other
133282	5	U52960	SRB7 (suppressor of RNA polymerase B; yeast) homolog	Other
100783	4.9	HG3748-HT4 D18	"Basic Transcription Factor, 44 Kda Subunit"	Other
122223	4.9	AA436158	ESTs	Other
104660	4.8	AA007160	ESTs	SS
113702	4.8	T97307	ESTs; Moderately similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	Other
101185	4.7	L19872	aryl hydrocarbon receptor	Other
105308	4.7	AA233744	ESTs	Other
107168	4.7	AA621540	ESTs	Other
101201	4.6	L22524	matrix metalloproteinase 7 (matrilysin; uterine)	SS
101809	4.5	M86849	"Homo sapiens connexin 26 (GJB2) mRNA, complete cds"	TM
101478	4.5	M23379	RAS p21 protein activator (GTPase activating protein) 1	Other
104695	4.5	AA012953	ESTs	Other
100365	4.4	D78611	mesoderm specific transcript (mouse) homolog	TM
126819	4.3	AA305536	"EST176522 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence."	Other
101880	4.3	M97925	defensin; alpha 5; Paneth cell-specific	SS
126838	4.2	AA858097	pigment epithelium-derived factor	Other
101684	4.2	M63256	cerebellar degeneration-related protein (62kD)	Other
117634	4.2	N36421	ESTs; Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
132109	4.1	AA599801	ESTs	Other
115054	4.1	AA252863	ESTs	Other
106553	4	AA454967	ESTs	Other
119717	3.9	W69134	ESTs	Other

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FIGURE 11 (CONT)
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PRIMEKEY	Fold Upregulated In Tumors	Exemplar Accession	Complete Title	ORF Structural Info
131945	3.9	M87339	replication factor C (activator 1) 4 (37kD)	Other
128790	3.9	AA281725	secreted frizzled-related protein 4	SS
120562	3.8	AA280036	ESTs; Weakly similar to W01A8.c [C.elegans]	SS
109517	3.7	D60799	ESTs	Other
102618	3.7	U65932	extracellular matrix protein 1	SS
108286	3.7	AA434441	frizzled (Drosophila) homolog 7	Other
133640	3.6	D83004	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)	Other
100335	3.6	D63391	platelet-activating factor acetylhydrolase; isoform Ib; gamma subunit (29kD)	Other
104720	3.6	AA018441	ESTs	Other
107348	3.6	U43701	ribosomal protein L23a	Other
134989	3.6	AA236324	ESTs; Weakly similar to IIII ALU CLASS A WARNING ENTRY IIII [H.sapiens]	SS
111345	3.6	N89820	ESTs	Other
107053	3.6	AA600147	ESTs; Weakly similar to Similar to NADH-cytochrome B5 reductase [C.elegans]	Other
107240	3.5	D59368	ESTs	Other
107129	3.5	AA620553	flap structure-specific endonuclease 1	Other
134846	3.5	AA431505	Homo sapiens mRNA for putative Sqv-7-like protein; partial	TM
101897	3.5	S58544	sperm associated antigen 1	Other
107151	3.5	AA821169	ESTs	Other
106012	3.4	AA411621	ESTs	Other
101950	3.4	S79219	propionyl Coenzyme A carboxylase; alpha polypeptide	Other
116844	3.4	H64938	ESTs	Other
128025	3.4	AA937173	ESTs	TM
106785	3.4	AA478597	leukemia associated gene 1; candidate tumor suppressor frequently deleted in B-cell chronic lymphocytic leukemia (B-CLL)	Other
104518	3.4	R09815	proteasome (prosome; macropain) 26S subunit; ATPase; 5	Other
117667	3.4	N39214	ser-Thr protein kinase related to the myotonic dystrophy protein kinase	Other
104954	3.3	AA074514	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]	Other
105372	3.3	AA236481	ESTs	Other
104896	3.3	AA054228	ESTs	Other
113485	3.3	T87863	ESTs	Other
127003	3.3	AA550806	ESTs; Weakly similar to (define not available 3882151) [H.sapiens]	TM
100305	3.3	D50487	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase)	SS
134722	3.2	W47183	ESTs; Weakly similar to IIII ALU SUBFAMILY SB2 WARNING ENTRY IIII [H.sapiens]	Other
126801	3.2	AA512902	ESTs	SS, TM
133503	3.2	M33195	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	SS, TM
132183	3.2	L18183	Human MAC30 mRNA; 3' end	TM
105298	3.2	AA233459	ESTs	TM
111046	3.2	N55514	ESTs; Moderately similar to IIII ALU SUBFAMILY SP WARNING ENTRY IIII [H.sapiens]	TM
135309	3.2	D25984	ESTs	SS
102808	3.2	U90426	nuclear RNA helicase; DEAD variant of DEAD box family	Other
100552	3.1	HG2167-HT2 237	Protein Kinase H131, Camp-Dependent"	Other
127652	3.1	AA804487	ESTs	Other

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FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
118127	3.1	AA459703	ESTs; Moderately similar to coded for by C. elegans cDNA CEESD64F [C.elegans]	TM
131904	3.1	AA143019	ESTs; Highly similar to surface 4 integral membrane protein [H.sapiens]	TM
126547	3.1	U47732	transmembrane 4 superfamily member 3	Other
102823	3.1	U90914	carboxypeptidase D	SS
132298	3.1	N41849	Homo sapiens cytokine receptor related protein 4 (CYTOR4) mRNA; complete cds	Other
127445	3.1	AA906286	ESTs	Other
134395	3.1	L08717	lysosomal-associated membrane protein 2	SS, TM
105743	3.1	AA293300	ESTs; Weakly similar to semaphorin C [M.musculus]	Other
125827	3.1	A1471525	YY1 transcription factor	Other
101229	3.1	L27943	cytidine deaminase	Other
102306	3	U33317	defensin; alpha 6; Paneth cell-specific	SS
107318	3	T74445	"yc42B.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:2242 5', mRNA sequence"	Other
120983	3	AA398209	EST	Other
134700	3	AA481414	golgi SNAP receptor complex member 1	TM
131216	3	D31058	ESTs	SS
127565	3	D79516	"HUM272B04B Human aorta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-272B04 5', mRNA sequence."	Other
106882	2.9	AA489009	ESTs	Other
130874	2.9	T08287	ESTs	Other
101275	2.9	L37936	Ts translation elongation factor; mitochondrial	Other
111179	2.9	N67239	ESTs	Other
126086	2.9	H70975	"yr73g01.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:210960 5', mRNA sequence."	Other
105365	2.9	AA236275	ESTs	Other
118789	2.9	N75416	ESTs	Other
115117	2.9	AA256482	H.sapiens PAP mRNA	Other
100484	2.9	HG1103-HT1 103	"Guanine Nucleotide-Binding Protein Rai, Ras-Oncogene Related"	Other
101300	2.9	L40391	Homo sapiens (clone s153) mRNA fragment	Other
103075	2.9	X59543	ribonucleotide reductase M1 polypeptide	Other
132184	2.8	U84573	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	Other
106716	2.8	AA464962	ESTs	Other
134098	2.8	X06323	Human MRL3 mRNA for ribosomal protein L3 homologue (MRL3	Other
134485	2.8	X82153	cathepsin K (pycnodysostosis)	SS
128634	2.8	AA150726	ESTs	Other
112207	2.8	R49602	ESTs	Other
124904	2.8	R86970	ESTs	Other
125471	2.8	AA477571	UDP-glucose ceramide glucosyltransferase	SS
132180	2.8	AA405569	fibroblast activation protein; alpha	SS
104454	2.8	M84443	galactokinase 2	TM
134282	2.8	T25508	ESTs	Other
101558	2.8	M32011	neutrophil cytosolic factor 2 (85kD; chronic granulomatous disease; autosomal 2)	Other
130529	2.8	AA173238	small inducible cytokine A5 (RANTES)	Other
101804	2.7	M86699	TTK protein kinase	Other

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FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
109565	2.7	F01930	ESTs	Other
112427	2.7	R62604	ESTs	Other
116188	2.7	AA261819	ESTs	Other
121831	2.7	AA425374	ESTs	Other
132454	2.7	W78726	ESTs; Highly similar to serine/threonine kinase [H.sapiens]	Other
116399	2.7	AA599729	Homo sapiens homeobox protein A10 (HOXA10) gene; complete cds	Other
100409	2.7	D86957	Human mRNA for KIAA0202 gene; partial cds	Other
130987	2.7	R45698	ESTs	Other
107217	2.7	D51095	ESTs	SS, TM
125698	2.6	AA748483	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene; partial cds; neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes; complete cds	SS
118722	2.6	N73563	ESTs	SS
104521	2.6	R11604	"Y47c1.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:132 5', mRNA sequence"	Other
130800	2.6	AA223386	ESTs; Weakly similar to katanin p80 subunit [H.sapiens]	Other
134415	2.6	AA329274	protein tyrosine phosphatase type IVA; member 2	TM
116461	2.6	AA621557	ESTs; Moderately similar to HIII ALU SUBFAMILY SQ WARNING ENTRY HIII [H.sapiens]	Other
100864	2.6	HG4297-HT4 567	Transcriptional Coactivator Pca4	Other
103818	2.6	AA150614	"Z143h5.r1 Soares_pregnant_uterus_NoHPU Homo sapiens cDNA clone IMAGE:54729 5', mRNA sequence"	Other
105713	2.6	AA291321	ESTs	Other
114969	2.6	AA250775	ESTs	Other
130415	2.6	X07290	Human HF.12 gene mRNA	Other
101791	2.6	M83822	Human belge-like protein (BGL) mRNA; partial cds	Other
128131	2.6	A1283162	claudin 3	SS, TM
131564	2.6	AA491465	ESTs	Other
100279	2.6	D42084	Human mRNA for KIAA0094 gene; partial cds	Other
130149	2.6	J04031	methylenetetrahydrofolate dehydrogenase (NADP+ dependent); methylenetetrahydrofolate cyclohydrolase; formyltetrahydrofolate synthetase	Other
119888	2.6	W81710	ESTs	SS
126638	2.6	AA649257	ESTs	Other
131672	2.6	X12901	Human mRNA for villin	Other
134405	2.6	J04177	collagen; type XI; alpha 1	Other
101188	2.5	L20320	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	TM
104534	2.5	R22303	ESTs; Weakly similar to putative p150 [H.sapiens]	Other
135178	2.5	U43747	Friedreich ataxia	SS
124308	2.5	H93575	ESTs	SS
125621	2.5	A1051602	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	TM
101342	2.5	L76191	interleukin-1 receptor-associated kinase 1	Other
129351	2.5	AA167268	ESTs	Other
103774	2.5	AA092898	ESTs; Weakly similar to R07G3.6 [C.elegans]	Other
131289	2.5	AA495697	ESTs	SS, TM
132094	2.5	W01996	ESTs; Highly similar to (define not available 4929683) [H.sapiens]	Other
103223	2.5	X74801	chaperonin containing TCP1; subunit 3 (gamma)	Other

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FIGURE 11 (CONT)
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
105810	2.5	AA279991	ESTs	Other
115719	2.5	AA416997	ESTs	Other
134888	2.5	AA148094	Tat-Interacting protein (30kD)	Other
105564	2.5	AA262943	ESTs	Other
128689	2.5	AA130158	ESTs	Other
103391	2.5	X94453	pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)	Other
104182	2.5	AA479990	ESTs; Weakly similar to glioma amplified on chromosome 1 protein [H.sapiens]	SS, TM
123494	2.5	AA599786	ESTs	Other
122905	2.5	AA470070	ESTs	Other
109175	2.5	AA180496	ESTs	Other
129907	2.5	D80170	ESTs	Other
115142	2.4	AA258116	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
125474	2.4	AA151216	Homo sapiens 14-3-3 protein mRNA; complete cds	SS
125745	2.4	AJ283493	ribophorin II	Other
100103	2.4	AF007875	dolichyl-phosphate mannosyltransferase polypeptide 1; catalytic subunit	Other
102887	2.4	U73379	Human cyclin-selective ubiquitin carrier protein mRNA; complete cds	Other
133170	2.4	U21049	epithelial protein up-regulated in carcinoma	SS, TM
109141	2.4	AA176428	ESTs	Other
132811	2.4	U25435	transcriptional repressor	Other
102862	2.4	X01057	Interleukin 2 receptor, alpha	SS, TM
104300	2.4	D37933	syntaxin 1B	Other
105091	2.4	AA146859	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Other
110874	2.4	H89315	"yw25e09.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253288 3', mRNA sequence."	TM
122571	2.4	AA452600	EST	Other
123421	2.4	AA598440	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	Other
132181	2.4	AA046939	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	Other
128445	2.4	AA306121	ESTs	SS
113923	2.4	W80763	ESTs; Moderately similar to FK506-binding protein 65kD [M.musculus]	Other
100598	2.4	HG2463-HT2 559	Guanine Nucleotide-Binding Protein G25k	Other
130869	2.4	AA128100	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	Other
132393	2.4	W85888	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
100830	2.4	HG4074-HT4 344	Rad2	Other
133765	2.4	D21255	cadherin 11 (OB-cadherin; osteoblast)	SS, TM
100867	2.4	HG4316-HT4 588	Transketolase-Like Protein	Other
119859	2.4	W80702	ESTs	Other
135269	2.4	M77698	YY1 transcription factor	Other
115140	2.4	AA258030	ESTs; Weakly similar to (define not available 3874821) [C.elegans]	Other
102162	2.4	U18291	CDC16 (cell division cycle 16; S. cerevisiae; homolog)	Other

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FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
100372	2.4	D79997	KIAA0175 gene product	TM
106981	2.4	AA521157	ESTs	Other
130114	2.4	AA234717	ESTs	Other
116129	2.3	AA459956	ESTs	Other
122235	2.3	AA436475	ESTs	Other
107315	2.3	T62771	Homo sapiens nucleoplasmin-3 (NPM3) mRNA; complete cds	SS
125905	2.3	T69868	chaperonin containing TCP1; subunit 2 (beta)	Other
133061	2.3	AB000584	prostate differentiation factor	SS
107531	2.3	Y13936	protein phosphatase 1G (formerly 2C); magnesium-dependent; gamma isoform	Other
125820	2.3	AA730136	teratocarcinoma-derived growth factor 1	Other
131725	2.3	AA456264	ESTs; Highly similar to (define not available 4176448) [H.sapiens]	Other
101228	2.3	L27706	chaperonin containing TCP1; subunit 6A (zeta 1)	Other
132571	2.3	R84594	ESTs; Highly similar to (define not available 4809026) [H.sapiens]	SS, TM
100090	2.3	AC002486	"Human BAC clone RG367O17 from 7p15-p21, complete sequence [Homo sapiens]"	Other
103658	2.3	Z74815	collagen; type I; alpha 1	SS, TM
104897	2.3	AA054641	ESTs	Other
106818	2.3	AA480890	ESTs	Other
113077	2.3	T40442	ESTs	SS
128773	2.3	M28879	granzyme B (granzyme 2; cytotoxic T-lymphocyte-associated serine esterase 1)	SS
129506	2.3	AA258286	Homo sapiens mRNA for KIAA0877 protein; partial cds	TM
133746	2.3	U44378	MAD (mothers against decapentaplegic; Drosophila) homolog 4	Other
134272	2.3	X76040	Lon protease-like protein	Other
106267	2.3	AA431873	Homo sapiens clone 24711 mRNA sequence	Other
133493	2.3	AA284143	Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA; complete cds	Other
104278	2.3	C02582	ESTs; Highly similar to (define not available 5114045) [H.sapiens]	Other
127211	2.3	AA480935	"aa28c03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814564 5', mRNA sequence."	Other
110721	2.3	H97678	ESTs	Other
114774	2.3	AA150043	ESTs	TM
132968	2.3	N77151	Homo sapiens mRNA for KIAA0799 protein; partial cds	Other
106916	2.3	AA490814	ESTs	Other
113849	2.3	W60439	ESTs; Moderately similar to cbp146 [M.musculus]	Other
131028	2.3	U20240	CCAAT/enhancer binding protein (C/EBP); gamma	Other
130380	2.3	U55853	Homo sapiens 130 kD Golgi-localized phosphoprotein (GPP130) mRNA; complete cds	SS
125390	2.3	H95094	KIAA0016 gene product	SS, TM
127256	2.3	AA327550	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
132116	2.3	AA234767	ESTs	SS, TM
117765	2.3	N47797	ESTs	Other
119126	2.3	R45175	ESTs	Other
129482	2.2	AA435849	ESTs; Moderately similar to unknown protein [H.sapiens]	Other
120493	2.2	AA255933	ESTs	SS
108927	2.2	AA143493	ESTs; Weakly similar to PLECKSTRIN [H.sapiens]	Other

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FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
122520	2.2	AA449427	ESTs; Moderately similar to pregnancy-specific beta-1 glycoprotein 2 [H.sapiens]	Other
125982	2.2	R98091	RAE1 (RNA export 1; S.pombe) homolog	Other
132325	2.2	N37065	ESTs; Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
100287	2.2	D43950	Human mRNA for KIAA0098 gene; partial cds	Other
114895	2.2	AA236177	Homo sapiens mRNA for KIAA0887 protein; partial cds	Other
105038	2.2	AA130273	ESTs; Weakly similar to (define not available 4240269) [H.sapiens]	Other
105476	2.2	AA255473	ESTs	SS
106942	2.2	AA496347	ESTs; Highly similar to gene 7442 protein [H.sapiens]	Other
110566	2.2	H59990	ESTs	Other
111068	2.2	N58397	ESTs	Other
127963	2.2	A1299013	"qn13h12.x1 NCI_CGAP_LuS Homo sapiens cDNA clone IMAGE:1898183 3' similar to TR:O22813 OZ2813 PUTATIVE NAD(P)-DEPENDENT CHOLESTEROL DEHYDROGENASE. ", mRNA sequence."	TM
130985	2.2	AA243700	ESTs	Other
132877	2.2	R40685	Homo sapiens mRNA for KIAA0851 protein; complete cds	TM
135242	2.2	M74093	cyclin E1	TM
129468	2.2	J03040	secreted protein; acidic; cysteine-rich (osteonectin)	SS
132616	2.2	AA386264	ESTs	SS, TM
133780	2.2	M14219	decorin	Other
121853	2.2	AA425887	ESTs	Other
114608	2.2	AA079381	ESTs	Other
129017	2.2	H13108	ESTs	SS
132725	2.2	L41887	splicing factor; arginine/serine-rich 7 (35kD)	Other
125606	2.2	R28463	ESTs	SS
105538	2.2	AA258860	ESTs; Highly similar to (define not available 4583654) [H.sapiens]	Other
133221	2.2	AA235289	ESTs; Highly similar to rap2 gene product [H.sapiens]	Other
106389	2.2	AA446949	ESTs	Other
128949	2.2	AA190993	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	Other
120969	2.2	AA398116	ESTs	Other
102495	2.2	U51240	Human mRNA for KIAA0085 gene; partial cds	TM
101124	2.2	L10343	protease inhibitor 3; skin-derived (SKALP)	SS
102778	2.2	U83463	syndecan binding protein (syntenin)	Other
107307	2.2	T52099	creatine kinase; mitochondrial 2 (sarcomeric)	Other
111605	2.2	R11638	ESTs	Other
101959	2.2	S80343	arginyl-tRNA synthetase	Other
101031	2.2	J05070	matrix metalloproteinase 9 (gelatinase B; 92kD gelatinase; 92kD type IV collagenase)	SS
131701	2.2	AA149008	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
105344	2.2	AA235303	ESTs	TM
103166	2.2	X67951	proliferation-associated gene A (natural killer-enhancing factor A)	Other
131463	2.2	X74142	forkhead (Drosophila)-like 1	Other
131412	2.2	U34044	Human selenium donor protein (selD) mRNA; complete cds	Other
134982	2.2	N46086	ESTs	Other
127236	2.1	A1341818	budding uninhibited by benzimidazoles 1 (yeast homolog)	Other
104459	2.1	M91493	EST	Other

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FIGURE 11 (CONT)
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
124596	2.1	N70088	ESTs	Other
105650	2.1	AA282347	ESTs; Highly similar to (define not available 4454694) [H.sapiens]	Other
134917	2.1	X87241	FAT tumor suppressor (Drosophila) homolog	SS
132478	2.1	H20606	Homo sapiens mRNA for KIAA0746 protein; partial cds	SS, TM
134484	2.1	N79354	ESTs; Weakly similar to Rga [D.melanogaster]	Other
111221	2.1	N68869	ESTs	Other
100892	2.1	HG4557-HT4 962	"Small Nuclear Ribonucleoprotein U1, 1snrp"	Other
117170	2.1	H98153	ESTs	Other
124049	2.1	F10523	primase; polypeptide 2A (58kD)	Other
131692	2.1	D50914	Human mRNA for KIAA0124 gene; partial cds	TM
103003	2.1	X52003	trifoli factor 1 (breast cancer; estrogen-inducible sequence expressed in)	SS
134085	2.1	U20979	chromatin assembly factor I (150 kDa)	Other
126216	2.1	N23870	ESTs	Other
102721	2.1	U79241	Human clone 23759 mRNA; partial cds	Other
128040	2.1	AA918528	ESTs	Other
101038	2.1	J05249	replication protein A2 (32kD)	SS
106060	2.1	AA417287	C-terminal binding protein 2	Other
103622	2.1	Z48042	basic transcription factor 3	Other
127884	2.1	AA768630	ESTs	Other
130911	2.1	W72906	HIRA interacting protein 4 (dnaJ-like)	Other
104260	2.1	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA; complete cds	Other
120714	2.1	AA292689	ESTs	Other
101578	2.1	M34423	galactosidase; beta 1	SS
113443	2.1	T66158	ESTs	SS
101516	2.1	M28249	Accession not listed in Genbank	Other
106480	2.1	AA450373	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY	Other
111385	2.1	N92659	ESTs	Other
121121	2.1	AA399371	ESTs; Weakly similar to (define not available 4688925) [H.sapiens]	Other
124768	2.1	R40177	ESTs	Other
102501	2.1	U51586	Human siah binding protein 1 (SiabBP1) mRNA; partial cds	Other
106432	2.1	AA448850	ESTs	Other
132812	2.1	R48108	ESTs	Other
125681	2.1	AA394176	accessory proteins BAP31/BAP28	TM
130511	2.1	L32137	cartilage oligomeric matrix protein	Other
128219	2.1	AA978333	ESTs	Other
130982	2.1	AA102051	transmembrane 4 superfamily member 6	SS, TM
101840	2.1	M93056	protease inhibitor 2 (anti-elastase); monocyte/neutrophil	TM
123928	2.1	AA621363	EST	Other
132073	2.1	N67408	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY	Other
101671	2.1	M61832	!!!! [H.sapiens]	Other
107059	2.1	AA608545	S-adenosylhomocysteine hydrolase	Other
132791	2.1	AA446088	ESTs	Other
103131	2.1	X65614	ESTs; Weakly similar to YY1-associated factor 2 [H.sapiens]	Other
104791	2.1	AA029046	S100 calcium-binding protein P	Other
			ESTs	Other

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FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
135181	2.1	AA621349	ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like [C.elegans]	Other
104334	2.1	D82614	ESTs	Other
132103	2.1	AA025086	ESTs	Other
126743	2.1	AA179253	poly(A)-binding protein-like 1	Other
100439	2.1	D87453	Human mRNA for KIAA0264 gene; partial cds	Other
114860	2.1	AA235112	ESTs; Moderately similar to similar to murine RNA-binding protein [H.sapiens]	Other
116732	2.1	F13779	ESTs; Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	Other
131045	2.1	H30863	ESTs; Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canal protein. [H.sapiens]	Other
133209	2.1	AA114183	ESTs; Moderately similar to glutamate pyruvate transaminase [H.sapiens]	Other
101758	2.1	M77836	Human pyrroline 5-carboxylate reductase mRNA; complete cds	Other
102214	2.1	U23752	SRY (sex-determining region Y)-box 11	Other
130100	2.1	AA425593	ESTs	Other
109799	2.1	F10770	Homo sapiens clone 669 unknown mRNA; complete sequence	Other
130860	2.1	U66061	T-cell receptor; beta cluster	SS, TM
106685	2.1	AA461551	ESTs; Highly similar to 73 kDa subunit of cleavage and polyadenylation specificity factor [H.sapiens]	TM
125724	2.1	AA083407	stimulated trans-acting factor (50 kDa)	Other
134258	2.1	L28010	heterogeneous nuclear ribonucleoprotein F	Other
129642	2.1	R50008	7-dehydrocholesterol reductase	TM
125336	2.1	T86823	ESTs	Other
125303	2	Z39821	ESTs	Other
100749	2	HG3521-HT3 715	Ras-Related Protein Rho1b	Other
128185	2	AI393989	ESTs	TM
126880	2	AI151406	ESTs	SS, TM
105263	2	AA227926	ESTs	Other
123288	2	AA495836	EST	Other
105807	2	AA393803	ESTs	Other
105040	2	AA131047	KIAA0698 gene product	TM
131977	2	F09788	procollagen-proline; 2-oxoglutarate 4-oxoxygenase (proline 4-hydroxylase); alpha polypeptide II	SS
117992	2	N52000	ESTs	SS, TM
134037	2	X53586	Human mRNA for integrin alpha 6	SS
132744	2	X54326	glutamyl-prolyl-HRNA synthetase	Other
101581	2	M34996	"Human MHC cell surface glycoprotein (HLA-DQA) mRNA, 3'end"	SS, TM
103576	2	Z26317	desmoglein 2	SS
131235	2	AA223284	ESTs; Moderately similar to (define not available 4680395) [H.sapiens]	Other
127910	2	AA781881	ESTs; Weakly similar to sperm fertilization protein sp56 precursor [M.musculus]	SS
101552	2	M31642	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	Other
100318	2	AA436570	Homo sapiens mRNA for pre-mRNA cleavage factor I subunit	Other
101192	2	L20859	Human leukemia virus receptor 1 (GLVR1) mRNA; complete cds	TM
104592	2	R61003	Homo sapiens serine protease mRNA; complete cds	SS
129095	2	L12350	thrombospondin 2	SS

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FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
105705	2	AA290767	ESTs	Other
128461	2	M83262	arachidonate 5-lipoxygenase-activating protein	SS, TM

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Accession	Score	Accession	Description	Category
16074	>10	AA001507	ESTs	other
25047	>10	AA011031	ESTs	other
25082	>10	AA017257	ESTs	other
16490	>10	AA026418	ESTs	other
25179	>10	AA031288	H.sapiens mR	other
25215	>10	AA035540	APOLIPOPRO	other
25282	>10	AA044825	ESTs	other
16810	>10	AA053638	ESTs	other
16835	>10	AA054438	ESTs	SS,
10747	>10	AA055841	ESTs	other
10748	>10	AA055892	ESTs	other
16993	>10	AA065300	Human mRNA	other
17051	>10	AA070801	ESTs	TM
10840	>10	AA084104	ESTs	other
7296	>10	AA085661	ESTs	other
7325	>10	AA090842	ESTs Weakly	other
17419	>10	AA113349	EST	?
17541	>10	AA127459	ESTs	other
17559	>10	AA128407	ESTs	other
25669	>10	AA128978	ESTs	?
17600	>10	AA130596	ESTs	other
10992	>10	AA132523	Homo sapiens	other
17654	>10	AA133250	ESTs	TM
17734	>10	AA137246	ESTs	other
25801	>10	AA148530	EST - RC_AA	TM
25806	>10	AA149007	EST	?
11121	>10	AA156359	Human TAR D	?
11160	>10	AA164289	ESTs	other
25925	>10	AA164494	ESTs Weakly	other
25934	>10	AA165355	Human clone	?
17987	>10	AA169379	ESTs	other
18008	>10	AA171895	Homo sapiens	TM
33953	>10	AA173290	Human HOXA	other
33980	>10	AA180223	CAMP-DEPEN	other
34013	>10	AA190888	EST - RC_AA	other
34014	>10	AA191348	ESTs	other
34015	>10	AA191353	ESTs	TM
34070	>10	AA196549	ESTs	other
18260	>10	AA206801	ESTs	?
34105	>10	AA207123	ESTs	SS,
34107	>10	AA209469	ESTs	other
18330	>10	AA216722	Human mRNA	TM
18362	>10	AA223912	Ribonuclease	other
18392	>10	AA227751	ESTs	SS,
34188	>10	AA228030	ESTs	TM
34197	>10	AA232315	Homo sapiens	other
25948	>10	AA234365	Homo sapiens	?
25951	>10	AA234556	EST	?
11561	>10	AA236533	Evl-1	other
26059	>10	AA236685	ESTs	other
26100	>10	AA242835	Human mRNA	other
11603	>10	AA243052	ESTs Highly	other
7785	>10	AA243375	EST - AA2433	other
34372	>10	AA251973	ESTs	?
26240	>10	AA252282	Human mRNA	TM

FIGURE 12

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34382	>10	AA252512	ESTs	other
34391	>10	AA252703	EST - RC, AA	other
26274	>10	AA253011	ESTs	?
34400	>10	AA253400	ESTs	other
26291	>10	AA253422	ESTs	?
26355	>10	AA256379	ESTs	other
11813	>10	AA258158	ESTs	other
34518	>10	AA278721	ESTs	?
26545	>10	AA278979	ESTs	other
26574	>10	AA279504	ESTs	other
34554	>10	AA280016	DNA polymer	other
34581	>10	AA280298	ESTs	TM
26628	>10	AA280641	ESTs Highly	TM
11869	>10	AA280670	ESTs	SS.
34575	>10	AA280738	ESTs	TM
26677	>10	AA281636	ESTs	?
26700	>10	AA282197	EST	?
34672	>10	AA284372	ESTs	other
34692	>10	AA285079	ESTs	other
12143	>10	AA290991	ESTs	other
8092	>10	AA316272	ESTs	TM
34904	>10	AA321746	EST	other
8111	>10	AA323787	ESTs	other
8125	>10	AA330771	Human protein	TM
26918	>10	AA331393	ESTs	other
26926	>10	AA342402	ESTs	other
26935	>10	AA347193	ESTs Weakly	TM
35038	>10	AA350541	ESTs Moder	TM
35049	>10	AA350857	ESTs	other
35106	>10	AA371561	EST Weakly	?
35197	>10	AA398120	ESTs	other
35277	>10	AA398536	ESTs	other
35309	>10	AA398660	EST	other
35322	>10	AA398710	H. sapiens RN	TM
27037	>10	AA400198	ESTs	TM
35495	>10	AA400527	ESTs	?
27046	>10	AA400670	Homo sapiens	other
35500	>10	AA400715	ESTs	other
12480	>10	AA403116	Homo sapiens	other
35693	>10	AA405485	ESTs Weakly	other
35697	>10	AA405512	ESTs	other
35766	>10	AA406169	Homo sapiens	other
35769	>10	AA406206	ESTs	other
35798	>10	AA410231	ESTs	other
35801	>10	AA410291	ESTs	other
35803	>10	AA410295	ESTs	other
35822	>10	AA411144	ESTs	TM
35874	>10	AA412024	EST	?
35958	>10	AA412550	ESTs	other
36052	>10	AA417027	EST	TM
36258	>10	AA423952	ESTs Weakly	other
36288	>10	AA424502	ESTs	other
36307	>10	AA424803	EST	?
36371	>10	AA426017	ESTs	TM
36395	>10	AA428353	ESTs	other
36405	>10	AA426406	Homo sapiens	other

FIGURE 12
(cont.)

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36506	>10	AA429610	ESTs	other
36571	>10	AA430726	EST - RC_AA	SS,
36695	>10	AA433910	ESTs	other
36739	>10	AA435610	EST - RC_AA	?
36753	>10	AA435688	ESTs	other
36845	>10	AA436198	ESTs	?
13136	>10	AA436560	ESTs	SS, TM
13143	>10	AA436619	ESTs	SS,
36958	>10	AA442060	ESTs	other
36962	>10	AA442082	ESTs	?
36981	>10	AA442845	EST	?
13237	>10	AA443971	ESTs Weakly	?
13242	>10	AA445994	ESTs	other
37057	>10	AA446131	ESTs	other
37068	>10	AA446312	ESTs Weakly	other
37074	>10	AA446344	ESTs	SS,
37084	>10	AA446486	Homo sapiens	?
37135	>10	AA447540	EST	?
37159	>10	AA447714	EST - RC_AA	other
37168	>10	AA447772	ESTs	?
37246	>10	AA449311	Homo sapiens	other
37310	>10	AA451707	ESTs	other
37453	>10	AA454610	ESTs	?
37456	>10	AA454632	ESTs	TM
27787	>10	AA454660	ESTs	?
37492	>10	AA455248	EST - RC_AA	other
37546	>10	AA456641	ESTs	TM
37601	>10	AA458864	ESTs	other
37611	>10	AA458996	Human signal	SS, TM
37615	>10	AA459101	Human serine	other
37653	>10	AA460017	ESTs	other
37677	>10	AA460530	Homo sapiens	other
37777	>10	AA464860	Homo sapiens	other
8848	>10	AA465016	Homo sapiens	?
37816	>10	AA469954	EST	?
37829	>10	AA470084	ESTs	other
28015	>10	AA477421	ESTs	other
37978	>10	AA479294	EST - RC_AA	other
37979	>10	AA479295	ESTs Highly	other
37983	>10	AA479348	H.sapiens mR	other
14054	>10	AA485223	ESTs	TM
38121	>10	AA485724	EST - RC_AA	other
28122	>10	AA485928	ESTs Weakly	other
38167	>10	AA487207	EST - RC_AA	other
38172	>10	AA487424	EST - RC_AA	other
38179	>10	AA487492	Homo sapiens	other
38182	>10	AA487501	ESTs	other
38194	>10	AA487969	ESTs	other
28141	>10	AA488432	ESTs	?
38211	>10	AA488687	ESTs	other
38235	>10	AA489030	ESTs	other
38280	>10	AA489791	EST - RC_AA	other
38316	>10	AA490500	Homo sapiens	other
38330	>10	AA490882	ESTs	other
38456	>10	AA504343	ESTs	SS,
38460	>10	AA504462	ESTs	other

FIGURE 12
(cont.)

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38553	>10	AA521471	ESTs	other
38560	>10	AA598545	ESTs	?
38590	>10	AA598648	Human mRNA	other
38601	>10	AA598738	ESTs	?
28323	>10	AA599639	ESTs	other
38828	>10	AA609177	ESTs	TM
38838	>10	AA609215	EST - RC_AA	?
38867	>10	AA609318	Human cbl-b m	TM
38871	>10	AA609333	EST	?
38970	>10	AA609749	ESTs	other
38984	>10	AA609839	ESTs Modera	?
39045	>10	AA610077	ESTs	other
39062	>10	AA620333	EST	?
39080	>10	AA620552	EST - RC_AA	?
39110	>10	AA620709	ESTs Weakly	other
39176	>10	AA621091	ESTs	other
39218	>10	AA621330	ESTs	other
39221	>10	AA621346	Homo sapiens	other
39232	>10	AA621409	ESTs	other
21	>10	AB000905	H.sapiens hls	?
6963	>10	AFFX-HUMTFAFFX-HUMT		?
33890	>10	AFFX-HUMTFAFFX-HUMT		?
39302	>10	C14944	ESTs	other
39329	>10	C20797	EST	?
28644	>10	D12163	ESTs	other
218	>10	D13540	PROTEIN-TYR	other
236	>10	D13645	Human mRNA	other
9127	>10	D30037	PHOSPHATID	other
459	>10	D38293	Human mRNA	TM
39405	>10	D50975	ESTs	other
39433	>10	D52037	Human thymid	other
39438	>10	D52692	Human Ca2+	TM
14708	>10	D59388	EST	?
39488	>10	D60831	ESTs	other
39504	>10	D80632	ESTs	other
765	>10	D86096	Prostaglandin	?
787	>10	D86969	Human mRNA	other
789	>10	D86971	Human mRNA	other
39529	>10	F02202	ESTs	?
39535	>10	F02450	ESTs Modera	TM
18676	>10	F04022	ESTs	other
18718	>10	F04915	ESTs	other
18762	>10	F09458	ESTs	other
18782	>10	F09739	ESTs	other
29080	>10	F13655	ESTs Modera	other
19001	>10	H02890	ESTs	other
19184	>10	H10395	EST	?
39725	>10	H11323	ESTs	other
19203	>10	H11593	ESTs	other
19328	>10	H17808	ESTs	other
19387	>10	H20128	ESTs	?
39787	>10	H20131	ESTs	SS,
19389	>10	H20165	EST	?
39832	>10	H26279	EST - RC_H2	other
19591	>10	H40688	ESTs	other
29229	>10	H48459	Human mRNA	other

FIGURE 12
(cont.)

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19727	>10	H52702	ESTs	?
19787	>10	H56679	ESTs	other
39995	>10	H62474	EST	SS, TM
28331	>10	H68116	ESTs	TM
29344	>10	H68839	EST	?
40064	>10	H72283	Human mRNA	other
40083	>10	H73488	MITOCHOND	other
18949	>10	H78263	ESTs	TM
40204	>10	H88296	EST - RC_HB	other
28523	>10	H88353	ESTs Weakly	?
29551	>10	H90134	ESTs	?
29645	>10	H95840	ESTs	?
20057	>10	H98079	ESTs	other
976	>10	HG2036-HT20EST - HG2036		?
1158	>10	HG3344-HT3EST - HG3344		?
1210	>10	HG37-HT37	EST - HG37-H	?
1346	>10	HG4716-HT5EST - HG4716		?
1349	>10	HG4747-HT5EST - HG4747		?
1445	>10	J03027	MHC class I p	?
1570	>10	K01383	EST - K01383	?
1684	>10	L07541	Replication fa	other
1652	>10	L17328	Human FE22	TM
1856	>10	L18920	MELANOMA-A	?
1863	>10	L19161	TRANSLATIO	other
2070	>10	L37378	Homo sapiens	SS, TM
2123	>10	L40396	Homo sapiens	other
2144	>10	L41349	Phospholipase	SS,
9723	>10	L44542	ESTs	other
2188	>10	L47276	EST - L47276	other
2343	>10	M15353	Eukaryotic tra	other
2627	>10	M29610	Glycophorin E	TM
2857	>10	M58597	Fucosyltransfe	TM
3021	>10	M68941	Protein tyrosin	other
3183	>10	M84424	Cathepsin E	?
3196	>10	M86917	Oxysterol bind	other
20088	>10	N20054	ESTs Weakly	?
28795	>10	N20641	ESTs Highly	other
40427	>10	N21147	ESTs	other
40444	>10	N22140	ESTs Highly	other
28893	>10	N23003	ESTs	TM
40498	>10	N26086	Homo sapiens	SS,
40559	>10	N33024	ESTs	SS,
30190	>10	N33264	EST	?
30207	>10	N33920	H.sapiens mR	other
20304	>10	N34686	Homo sapiens	?
20307	>10	N34830	ESTs	other
30265	>10	N35115	ESTs	other
40594	>10	N35388	ESTs	other
40604	>10	N38893	Homo sapiens	other
40631	>10	N45124	ESTs	other
40660	>10	N49104	NUCLEAR FA	other
30810	>10	N50138	EST	?
30617	>10	N50646	ESTs	other
30831	>10	N50807	EST	?
30790	>10	N52935	EST	?
20584	>10	N55443	ESTs	TM

FIGURE 12
(cont.)

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40760	>10	N57927	ESTs Weakly	other
30938	>10	N58561	Cathepsin B	other
20614	>10	N59230	ESTs	SS,
20657	>10	N62889	ESTs	other
31136	>10	N63512	ESTs Weakly	TM
40827	>10	N64051	Homo sapiens	other
31310	>10	N66831	EST	?
40876	>10	N67607	Human Rho-d	other
20791	>10	N68057	Homo sapiens	?
40905	>10	N68738	ESTs	other
40911	>10	N69114	H.sapiens mR	other
40913	>10	N69218	ESTs	other
31484	>10	N69468	ESTs	other
31619	>10	N73449	ESTs	other
41005	>10	N79516	ESTs	TM
31818	>10	N89774	Homo sapiens	other
31872	>10	N91109	EST	other
41040	>10	N91948	ESTs	other
31944	>10	N93193	ESTs	other
41065	>10	N93618	ESTs	other
32034	>10	N98926	ESTs Modera	other
41107	>10	R01634	ESTs	other
41163	>10	R08176	ESTs	other
21238	>10	R08564	Plasminogen	other
21240	>10	R08613	ESTs	other
21412	>10	R20670	ESTs	other
21519	>10	R27975	EST - RC_R2	other
41381	>10	R42278	H.sapiens mR	?
32189	>10	R43183	ESTs	TM
32195	>10	R43471	ESTs Weakly	other
21902	>10	R43822	EST	?
21946	>10	R44707	ESTs	TM
22072	>10	R49406	ESTs	?
32240	>10	R50976	Ribonuclease	other
32258	>10	R55623	ESTs	other
22258	>10	R56432	ESTs	other
22282	>10	R59197	ESTs	other
32277	>10	R61493	Human mRNA	other
22372	>10	R62831	EST	?
22400	>10	R64109	ESTs	other
41593	>10	R64129	ESTs	other
10233	>10	R71427	ESTs Highly	other
41654	>10	R76437	THROMBOXA	TM
22557	>10	R76722	ESTs	other
22576	>10	R79111	ESTs	other
22593	>10	R79777	EST	?
41678	>10	R80675	EST	?
41719	>10	R89260	EST - RC_R0	other
22793	>10	R96208	ESTs	other
41752	>10	R97063	ESTs	other
3375	>10	S50223	HKR-T1	other
3406	>10	S66896	SQUAMOUS	other
3522	>10	S80267	Spleen tyrosio	other
41793	>10	T03887	ESTs	?
23198	>10	T40530	ESTs Weakly	other
23360	>10	T58531	ESTs	other

FIGURE 12
(cont.)

32635	>10	T61116	ESTs	other
42177	>10	T79786	ESTs	?
23623	>10	T84047	ESTs	?
23662	>10	T86674	ESTs	other
42242	>10	T89579	Homo sapiens	other
23759	>10	T90313	ESTs	other
23832	>10	T92018	ESTs	other
32740	>10	T92950	ESTs	other
42290	>10	T95105	ESTs	?
3598	>10	U01157	Glucagon-like	SS, TM
3659	>10	U04313	Protease inhib	other
3799	>10	U10690	Human MAG	?
3870	>10	U14518	Centromere p	other
3913	>10	U18261	Human MDA4	SS,
4029	>10	U21090	Human DNA p	other
4157	>10	U28811	Human cystei	other
4178	>10	U30246	Human burne	TM
15006	>10	U30246	Human burne	TM
4193	>10	U31116	Human beta-s	TM
4306	>10	U36798	Homo sapiens	TM
4362	>10	U39817	Bloom syndro	other
4386	>10	U40622	DNA repair pr	other
4388	>10	U40714	Human tyrosy	other
4455	>10	U43944	MALATE OXID	other
4477	>10	U45880	Human IAP-lik	other
4680	>10	U55766	Human Rev it	TM
4702	>10	U57341	EST - U57341	other
4713	>10	U57721	Human L-lym	other
4787	>10	U61145	Human enhan	other
4882	>10	U65437	Human homeo	?
4945	>10	U69108	Homo sapiens	other
4975	>10	U71088	Human MEK5	other
4994	>10	U72514	Human C2f m	other
5002	>10	U72761	Human karyop	other
5021	>10	U73524	Human putativ	TM
5149	>10	U79716	Human reelin	SS,
5214	>10	U83303	H. sapiens mR	?
5243	>10	U85946	Human brain s	other
32789	>10	W02779	ESTs Modera	other
42354	>10	W19348	ESTs	other
42390	>10	W40150	Homo sapiens	other
33006	>10	W46286	ESTs Weakly	TM
33020	>10	W46891	ESTs Weakly	other
33109	>10	W59961	Human mRNA	other
24197	>10	W67277	ESTs	other
24215	>10	W69425	ESTs	other
33301	>10	W73883	ESTs	other
33343	>10	W79834	ESTs Weakly	other
33377	>10	W81219	ESTs Weakly	other
42602	>10	W86423	ESTs	TM
33556	>10	W90705	Murine leukem	other
33616	>10	W93726	Protease Inhib	other
33666	>10	W95876	ESTs	TM
5510	>10	X05360	Cell division c	?
5558	>10	X07876	Wingless-type	SS,
5603	>10	X14253	Teratocarcino	TM

FIGURE 12
(cont.)

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5619	>10	X14850	HISTONE H2A	SS,
5623	>10	X14875	T-CELL SURF	?
5692	>10	X17644	G1 to S phase	other
5789	>10	X54925	Matrix metallo	other
5799	>10	X55330	Aspartylglucos	SS,
5802	>10	X55544	CYCLIC-AMP	?
5857	>10	X58377	Human mRNA	other
5960	>10	X63575	ATPase Ca++	TM
5963	>10	X63629	Cadherin 3 (R	SS, TM
5988	>10	X64810	Proprotein con	?
6041	>10	X87155	MITOTIC KIN	other
6095	>10	X69962	Fragile X mer	other
6106	>10	X70683	SRY (sex dete	TM
6155	>10	X74331	DNA primase	other
6167	>10	X74987	Ribonuclease	other
6188	>10	X76029	NEUROMEDI	TM
6315	>10	X81889	H.sapiens mR	other
6382	>10	X85133	H.sapiens RE	other
6384	>10	X63137	Human kines	other
6438	>10	X89398	URACIL-DNA	?
6449	>10	X89986	H.sapiens mR	TM
6478	>10	X91648	H.sapiens mR	SS, TM
6479	>10	X91653	EST - X91653	?
6494	>10	X92689	H.sapiens mR	TM
6713	>10	Y08564	EST - Y08564	?
6790	>10	Y12394	Homo sapiens	other
24915	>10	YEL003w	EST - YEL003	?
42773	>10	YEL019c/MM	EST - YEL019	?
24545	>10	Z38462	ESTs	other
33713	>10	Z38427	ESTs	other
33791	>10	Z40883	ESTs	other
42766	>10	Z69394	ESTs Modera	other
21558	>10	R33112	Human AF-6 m	other
26718	>10	AA282576	ESTs	?
40113	.9955090946	H78003	ESTs	?
10801	.9879448276	AA069285	ESTs Weakly	other
37491	.9513600842	AA455239	ESTs Highly	other
23900	.9272347693	T95789	ESTs	other
254	.9198395324	D14657	Human mRNA	other
6885	.8970927914	Z29331	Ubiquitin-con	other
29693	.8850766398	H97819	ESTs	SS,
26482	.8765189024	AA262491	ESTs	other
23123	.8699502035	T25306	EST	?
26525	.8160399123	AA278392	ESTs	other
13110	.7643356605	AA435840	Homo sapiens	other
34863	.7087597628	AA299784	EST	other
39432	.7034550083	D51691	Phosphoribos	?
31312	.6513325388	N68845	ESTs Weakly	?
21112	.6358446349	R01179	ESTs	?
31572	.6254820695	N71294	ESTs	other
17903	.6221229759	AA160259	EST	?
20747	.6094813734	N66842	ESTs	other
4676	.589223908	U55206	Homo sapiens	TM
34363	.5627081023	AA251587	Homo sapiens	other
39094	.540768988	AA620636	ESTs	other
3888	.5372009133	U15128	Human beta-	?

FIGURE 12
(cont.)

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39386	9.506250529	D12184	ESTs	TM
7874	4458059039	AA203742	ESTs	other
4192	4329744134	U31099	Human DP pr	TM
4507	9.422874945	U47050	Human putativ	TM
35606	9.412026255	AA402227	ESTs Modera	other
4970	3649551013	U70862	Human nuclea	?
18829	3432151573	H58813	EST	?
14837	2878584141	T40145	ESTs	TM
17336	2822148679	AA099585	ESTs	other
40541	2532836505	N30160	ESTs	other
29496	2487643833	H85434	EST	?
29943	1797074262	N24786	ESTs Modera	TM
17097	1829681314	AA169633	EST	other
21320	1243463318	R11673	ESTs	other
13883	1178796537	AA476917	ESTs Weakly	other
30539	0886887776	N49072	ESTs	other
32778	0877919549	W02063	EST	?
26380	0809559378	AA257012	EST	?
15888	0595893607	X95632	Human Abl in	other
40812	0012874244	N63419	ESTs	other
903	9640387906	D90070	ATL-derived P	other
22674	9515777733	R87180	ESTs	TM
40807	9510132281	N62995	TRANSCRIP	other
15244	9195644974	W00904	ESTs	TM
32296	8658776587	R67075	Zinc finger pro	other
18289	8575656789	AA209487	ESTs	other
19662	8507626284	H47391	ESTs	other
41607	833925517	R67868	CLEAVAGE S	other
2548	8299864699	M25897	Platelet factor	TM
7736	8279341243	AA232121	Human tyrosy	other
34490	7844537273	AA262354	ESTs	other
38658	7669313482	AA599477	ESTs	other
7528	8.765157554	AA149543	ESTs	other
39939	7555031142	H53454	EST - RC_H5	other
25111	7232692309	AA020787	ESTs	other
21655	8.716167279	R38239	EST	?
39663	8.665982852	H04756	ESTs Highly	other
1042	8.652112324	HG2510-HT2	EST - HG2510	?
32330	6361115426	R77776	ESTs	other
25382	6239456487	AA059007	ESTs	other
27074	5900813078	AA401475	ESTs Weakly	SS,
3955	5298909183	U18259	MHC class II	other
4959	8.52646827	U70322	Human transp	other
2315	5259185808	M14123	EST - M14123	?
37253	4896914632	AA449357	ESTs	other
39624	8.471316877	F10836	ESTs	?
23213	4569920887	T40891	ESTs	?
2788	8.453596435	M54995	Connective tis	TM
41154	4413390141	R07490	ESTs	?
32479	4093689549	T16282	WEE1-LIKE P	other
41251	3587565415	R28279	Human clone	other
19081	3583603183	H06701	ESTs Weakly	other
21098	3105927559	R00545	ESTs	other
14723	3061679053	D59894	ESTs	other
37154	2994822341	AA447666	Human CENP	other
8068	2835586361	AA313387	ESTs Highly	other

FIGURE 12
(cont.)

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7485	8.281679348	AA129547	ESTs	other
16501	.2517969834	AA026969	ESTs	other
34527	.2419163754	AA279091	ESTs	other
8700	.1948675663	Y07867	H.sapiens mR	other
2852	.1928816537	M58460	Human 75-kD	other
11188	.1862492488	AA172372	ESTs	TM
42293	8.183311084	T95333	ESTs Weakly	TM
5443	.1763317544	X02530	Interferon (gam	SS,
40937	.1534810594	N70607	ESTs	TM
23371	.1499496068	T69505	EST - RC_T59	?
26272	.1339974519	AA252981	ESTs Weakly	other
17306	.1332403762	AA086201	ESTs	other
18497	.1192326373	AA233795	ESTs	other
235	.0944363901	D13644	Human mRNA	other
24525	.0860187097	Z38347	ESTs	TM
7826	.0750029554	AA248884	EST - AA2488	TM
32142	.0739258775	R38715	Homo sapiens	other
39067	.0557768803	AA620405	ESTs	other
6235	.0448957236	X78416	Casein alpha	TM
29517	.0017588725	H88261	ESTs	other
28570	.9852455973	C21104	Homo sapiens	other
39344	.9182087762	C21034	ESTs Modera	other
18951	.9002189759	H00580	ESTs	other
18953	.8709160227	H00615	ESTs	other
18376	.8564099916	AA228925	ESTs	other
19830	7.847878447	H58911	ESTs	other
36023	7.840835828	AA416881	ESTs	other
13347	.8344414518	AA449238	ESTs	other
35614	.8284591351	AA431466	ESTs	other
2192	.8254072032	L48211	Homo Sapien	?
33016	.8006574068	W46577	H.sapiens mR	other
17215	.7941954036	AA083044	ESTs	other
34894	.7659738105	AA311881	EST	?
40614	7.695001222	N39257	ESTs	other
36295	.6834749899	AA424534	ESTs	other
19584	.6744302788	H38833	ESTs	TM
16914	.6686405336	AA058665	ESTs	SS,
35967	.6378079107	AA412694	Human splicin	other
21672	.6384823402	R38835	ESTs	other
19918	.6303275831	H69787	ESTs	?
10511	.6297744492	AA024482	ESTs Highly	other
17721	.6057911016	AA136590	ESTs	?
42302	.6031859697	T96130	EST	SS,
26134	.6000619383	AA243763	ESTs	other
18768	.5621789008	F09497	ESTs	other
34492	7.501590494	AA262439	ATL-derived P	other
270	.4512152125	D14822	EST - D14822	other
35975	.4177746986	AA412738	ESTs	other
29842	.4095809971	N21688	ESTs	?
35389	.3913043319	AA395555	ESTs	other
19979	.3868157166	H88477	ESTs	other
5793	.3865664025	X54942	CDC28 protei	other
19978	7.3809697151	H87770	EST - RC_H8	other
1280	.3691089318	HG4126-HT4	EST - HG4126	?
31571	.3676263454	N71250	ESTs	other
23765	.3541191734	T90443	ESTs Weakly	?

FIGURE 12
(cont.)

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35123	.3397833453	AA380927	EST	?
38252	.3341119467	AA489247	ESTs	other
38216	.3282021037	AA488861	ESTs	other
29418	.2489407005	H77915	EST - RC_H7	?
4834	.1980951054	U63541	Human mRNA	other
42504	.1913036522	W69803	ESTs	other
6111	.7.158000198	X71125	HM.sapiens mR	TM
41773	.7.154479618	T03024	ESTs Weakly	other
9951	.1363626363	N71513	ESTs	other
28109	.0941968224	AA485212	ESTs	other
988	.0783044653	HG2160-HT2	EST - HG2160	?
29848	.0610688511	N22107	ESTs	other
30628	.0607950168	N50744	ESTs	other
22567	.0225726353	R77771	ESTs	TM
9347	.7.0063230711	H03686	ESTs	TM
11695	.0026773299	AA252894	ESTs	other
40584	.0010096333	N34870	EST	?
193	.9767029188	D10923	PROBABLE G	TM
18305	.9740536051	AA214048	Collagen type	other
6078	.8699682397	X69141	FARNESYL-O	other
26741	.6.902658703	AA283198	ESTs	other
35069	.8992865685	AA358397	EST	?
23504	.8977135983	T71042	ESTs	other
299	.8824513025	D16815	Homo sapiens	other
40583	.8689903023	N34855	ESTs	other
31428	.8623762224	N68594	ESTs	other
6169	.8806959727	X75091	SET PROTEIN	other
39524	.856735517	F01905	MALATE OXID	other
34578	.8430689439	AA280837	ESTs	other
36678	.6.837527995	AA599920	Small inducib	other
23936	.8251471804	T96930	ESTs	other
9326	.8181321394	D89377	Msh (Drosoph	other
19188	.8067351968	H11255	ESTs Highly	TM
18185	.7882148811	AA194983	Homo sapiens	other
27028	.6.757529124	AA399630	ESTs Weakly	other
41289	.7519531681	R37265	EST	other
34511	.7364448798	AA278298	EST - RC_AA	other
1566	.7056207716	J05614	EST - J05614	?
25675	.6692299748	AA129757	ESTs Highly	other
5814	.6584342828	X56088	CYTOCHROM	SS,
13861	.6236291607	AA470145	ESTs	other
29794	.6026313353	N20598	ESTs	other
39333	.5902382643	C20910	Cyclin B1	other
3770	.5835303598	U09609	Nuclear factor	other
31831	.5829933764	N89894	ESTs	?
33063	.5808125028	W53000	Homo sapiens	other
20326	.5640084836	N35583	ESTs Weakly	?
34384	.5535703492	AA252537	ESTs	other
25599	.5490481991	AA114091	Human (clone	other
39749	.5369363254	H14988	ESTs	other
42596	.5200567072	W85900	ESTs	?
39606	.5119482185	F10243	ESTs Weakly	?
14617	.5105504748	C14983	ESTs	other
27831	.6.45670814	AA456044	ESTs	?
34896	.4496517783	AA312551	EST	?
27360	.4434305006	AA425356	ESTs	other

FIGURE 12
(cont.)

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20128	4326610424	N22015	ESTs	TM
6663	4324809977	Y00291	RETINOIC AC	TM
30692	4196036207	N51563	ESTs	other
36472	4189542265	AA428633	EST	?
9578	3961788753	H87652	Homo sapiens	other
39870	3818498156	H05826	ESTs	other
22697	3652792447	R89218	ESTs	other
37308	3647804993	AA451694	EST	TM
16101	3517262802	AA002147	EST	?
20629	3486854401	N59798	ESTs	other
36100	3364146287	AA417740	ESTs	?
15488	3252590241	W28097	Homo sapiens	other
36667	3131273544	AA432136	ESTs	other
30766	3115037924	N52627	EST - RC, N5	?
32882	2745311453	W37683	ESTs	TM
18072	2675797205	AA180448	EST	?
16231	2652604863	AA189747	Human mRNA	other
38282	2514165678	AA489814	EST	?
28125	6250317021	AA486073	ESTs	other
37484	2484456382	AA454747	ESTs	?
36818	1946328223	AA431478	ESTs	other
5082	1931116815	U78524	Human Gu b1	other
1441	1777287039	J02963	Integrin alpha	other
42105	614875944	T67710	ESTs	?
6061	1394863141	X68314	Glutathione pe	SS,
32570	1156028796	T30222	ESTs Weakly	TM
32504	1019612076	T17063	EST	?
23335	0977927504	T58804	EST	?
10867	0970991075	AA088458	ESTs Weakly	other
30883	0911993489	N56923	EST	?
14528	0859008453	AA620295	ESTs	TM
29454	0685955036	H81308	EST	?
6798	0539173276	Y13153	Homo sapiens	TM
21248	0525426545	R08871	ESTs	?
21940	0499964138	R44538	ESTs	?
29066	0455247653	F10927	Homo sapiens	other
18774	0446826953	F09609	ESTs	?
36722	0172343991	AA435512	ESTs	SS,
18062	0034342988	AA179845	ESTs Modera	other
22989	9992817406	T16305	ESTs	other
41745	9905623898	R95895	ESTs	?
8787	9894877658	AA504307	X-LINKED HE	other
20550	5984881795	N55013	ESTs	other
26470	9417764104	AA262179	ESTs	other
18574	9356497569	AA031926	EST	other
693	9169537389	D80007	Human mRNA	other
4093	5914830973	U25182	Human antiox	TM
1192	9086284407	HG3548-HT3	EST - HG3548	?
22956	8954735623	T10248	ESTs	other
36723	5891606409	AA435524	EST	?
2114	8844986595	L40384	EST - L40384	other
26872	5868238789	AA291137	ESTs	other
6602	8563883018	X98266	EST - X98266	other
42701	8594493433	Z38612	ESTs	other
28573	5845911116	C21118	ESTs	other
18290	8189427595	AA211901	ESTs	other

FIGURE 12 (cont.)

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732	.804391794	D83781	Human mRNA	other
5330	.801414561	U91327	EST - U91327	?
33503	.799071518	W88720	EST	?
2553	.779750586	M26167	Human platelet	?
34705	.785880625	AA286907	ESTs Weakly	other
42665	.759409104	W93659	ESTs	other
38180	.753931079	AA487495	EST - RC_AA	other
4244	.747673880	U33286	Human chrom	other
32822	.741895745	W16834	ESTs	TM
3977	.724588555	U18991	Retinal pigme	?
24673	.720236815	Z39301	ESTs	TM
6928	.712026112	Z46629	SRY (sex-dete	other
38726	.703079625	AA608733	ESTs	?
39290	.689237205	C14573	Human mRNA	other
11405	.681887379	AA232231	ESTs	other
22538	.679200659	R73567	Homo sapiens	TM
40747	.660539320	N56872	Homo sapiens	TM
31596	.655402460	N72094	ESTs	other
6329	.641565251	X82279	EST - X82279	?
31578	.627332366	N71361	ESTs	other
33207	.627181848	W70051	H.sapiens mR	other
2545	.610586014	M25753	Cyclin B1	other
22580	.598840264	R79156	ESTs	other
33592	.593531451	W93127	ESTs	other
28843	.573469875	D60252	ESTs	other
6160	.568905061	X74794	CDC21 HOMO	other
37987	.556134565	AA479666	ESTs	other
42515	.521786861	W72118	Homo sapiens	other
4732	.513066852	U58522	Human huntin	other
3299	.509985067	M95623	Hydroxymethyl	?
28320	.547340698	AA599574	ESTs	?
746	.547126089	D84454	Human mRNA	TM
39373	.463580495	C21517	ESTs	other
3117	.439841353	M81182	Peroxisomal m	other
21257	.434361244	R09196	ESTs Moderat	other
31487	.431864885	N69507	ESTs	other
28954	.413713051	F03153	ESTs	other
38828	.538978272	AA609595	ESTs	other
29903	.372232062	N23366	EST	?
30925	.343743231	N58295	ESTs Weakly	?
19091	.334461566	H07864	ESTs	TM
28209	.313895191	AA491250	ESTs	other
9470	.311889798	H40617	EST - H40617	other
9435	.307005665	H30201	EST - H30201	?
28552	.295443257	C20914	ESTs	other
27411	.294016426	AA428137	ESTs	other
30815	.292412526	N50556	ESTs	other
28313	.265797718	AA599309	ESTs	TM
39321	.264903538	C20632	ESTs	?
28934	.253104739	N24194	ESTs	other
1094	.249670312	HG2846-HT2	EST - HG2846	?
39578	.248112638	F08925	ESTs	TM
11232	.246679842	AA186804	ESTs Weakly	other
2466	.242634932	M21539	Human small	other
26843	.238775856	AA287450	ESTs	?
40331	.235338558	H97582	ESTs Weakly	other

FIGURE 12
(cont.)

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8035	.5205798365	AA305116	EST - AA3051	other
28793	.1955425722	N20593	ESTs Weakly	other
34109	.1481590107	AA210722	EST	?
26408	.1432577257	AA258177	ESTs Weakly	other
19263	.1427029807	H15054	ESTs	TM
24596	.1416089352	Z38810	ESTs	other
28589	.1365059753	C21245	H.sapiens mR	other
5684	.1121931412	X17098	Pregnancy-sp	other
30710	.1079347344	N51761	EST	?
35765	.0973514948	AA406167	EST	?
26360	.0863127861	AA256460	ESTs	?
2351	.0849612092	M15798	Proliferating C	?
30282	.0836877534	N35065	Homo sapiens	other
41792	.0737512465	T03866	ESTs	?
36710	.0703839864	AA434411	ESTs	other
39090	.0546885407	AA620628	ESTs	TM
42185	.0539926381	T79951	ESTs	?
18745	.0460321557	F09134	ESTs	other
35746	.0396841996	AA406063	ESTs	other
35356	.0354809581	AA399053	EST	?
38769	.0312706876	AA435750	EST	?
36900	.0279911548	AA436866	H.sapiens mR	other
27595	.0244757301	AA443326	ESTs	TM
16290	.0056611904	AA016145	ESTs	?
27117	.0016146599	AA405099	ESTs Weakly	other
4304	.9951954397	U36764	Eukaryotic tra	other
33458	.9907402027	W85835	Homo sapiens	other
26693	.9800909679	AA282120	EST	?
12669	.9758138651	AA417030	Homo sapiens	other
29701	.9708526387	H97970	EST	?
20480	.9557253836	N52168	ESTs	TM
8720	.9439110602	AA481218	EST - AA4812	other
34828	.9431269475	AA292436	Homo sapiens	SS, TM
14985	.9416210321	U15128	Human beta-	?
16115	.9377553523	AA004420	ESTs	?
42506	.9348587118	W70074	EST	other
34761	.9316837445	AA287833	ESTs	other
11870	.9281056201	AA262587	ESTs	TM
23211	.9258391854	T40889	ESTs	other
40611	.9160502275	N39138	Homo sapiens	other
42611	.9128605354	W87006	Homo sapiens	other
39652	.9045174605	H03099	ESTs	other
17581	.8896747511	AA129395	EST	?
37239	.8704375386	AA449121	ESTs	?
18712	.8703618781	F04677	ESTs	other
30709	.8611171953	N51752	ESTs Weakly	other
34179	.8503613948	AA227903	ESTs Highly	other
21433	.8256709888	R22183	EST	?
39731	.8186142741	H11760	ESTs	other
31295	.8116614607	N66653	ESTs	other
24647	.8041630555	Z39108	EST	?
31292	.8008871817	N66615	ESTs	other
1285	.7997542393	HG4157-HT4	EST - HG4157	?
1106	.7932425858	HG2981-HT3	EST - HG2981	?
18212	.7912262565	AA196506	ESTs	other
34367	.7822070451	AA251758	Homo sapiens	other

FIGURE 12
(cont.)

34802	.7797760205	AA291468	ESTs	TM
34762	.7775301546	AA287834	ESTs	other
11595	.7696612848	AA242819	ESTs	other
8285	.7639839111	AA405082	ESTs	?
17622	4.758835578	AA131584	ESTs Weakly	other
35781	.7572463523	AA406335	ESTs	other
34754	.7483874972	AA287642	Human mRNA	other
23237	.7444854356	T47291	EST	?
37667	.7280445357	AA460318	ESTs Highly	other
11568	.7257189975	AA236786	ESTs	other
38622	.7190695733	AA598967	ESTs	?
5137	.7057359474	U79296	Dihydrolipoam	other
25038	.7002244728	AA010065	CDC28 prote	other
19288	.7000147312	H16587	ESTs	other
32503	.6979488292	T17045	Collagen type	other
3278	.6953739298	M94055	SODIUM CHA	TM
8696	.6942061018	L38961	Integral trans	TM
35400	.6901390898	AA399591	Homo sapiens	other
35246	.6862691303	AA398367	EST Weakly	?
36387	.6822499271	AA426270	ESTs	other
21509	.6730072542	R27314	ESTs	other
31381	.6728672124	N87889	ESTs	other
26723	.6727894925	AA282781	ESTs Highly	other
36326	.6703621086	AA425151	Human GAP S	other
17409	.6688418667	AA113136	EST - RC_AA	other
4908	.6552339935	U67156	Human mitoge	other
30594	.6496238328	N49967	ESTs	other
38286	4.64639735	AA489847	ESTs Weakly	?
13073	.6426509458	AA433950	ESTs	other
40435	.6240181068	N21814	Homo sapiens	other
14474	.6226694379	AA609427	ESTs Moder	other
38213	4.6153099071	AA488847	ESTs Weakly	?
5312	4.6066441198	U90716	Human cell su	SS, TM
24225	.6041550359	W70328	ESTs	?
35588	.5868982366	AA401750	EST	?
29739	.5863199051	H99626	EST	?
7203	.5792992577	AA053096	EST - AA0530	other
2157	.5772055868	L41939	Homo sapiens	SS, TM
32086	.5661024279	R11510	ESTs	?
8085	.5648114738	AA314779	ESTs Weakly	SS,
224	.5622018898	D13633	Human mRNA	other
34006	.5609980241	AA188781	DNA polymera	other
33656	.5557384389	W95477	ESTs	other
34065	.5537335124	AA195517	ESTs Weakly	TM
6028	.5357922097	X66503	Adenylosuccin	other
4166	.5032930671	U29463	Cytochrome B	?
40262	.5024727522	H93562	ESTs	TM
22687	.5018672549	R88209	ESTs	TM
41069	.4977510482	N93969	H.sapiens mR	SS,
8264	.4793100575	AA401334	ESTs	other
27588	4.4720172971	AA443187	ESTs	other
35882	.4717597552	AA412047	ESTs	?
34479	4.4655191911	AA262080	Human bumet	TM
15921	.4548516438	Y12065	Homo sapiens	?
11279	.4380038671	AA195399	ESTs	other
39222	.4367650786	AA621348	ESTs Highly	other

FIGURE 12
(cont.)

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34428	.4364736768	AA256528	ESTs	other
8771	4.432067373	AA491188	ESTs	other
22193	.4189810024	R53891	Homo sapiens	other
7898	.4066170674	AA263032	ESTs	other
19902	.3886145805	H86736	ESTs	other
9278	.3888095205	D82374	ESTs	other
10716	.3794529068	AA053319	ESTs	TM
13183	.3751913512	AA442763	ESTs Highly	other
5690	.3723059412	X17620	NUCLEOSIDE	other
35102	4.37147138	AA371509	EST - RC_AA	TM
17983	.3612985467	AA159226	ESTs	other
24982	.3497206925	AFFX-HUMT	AFFX-HUMT	?
31680	.3416539668	N74438	ESTs	other
27168	4.3303068894	AA410258	ESTs	other
28731	.3231846655	D20981	EST	?
28348	.3212284906	AA608752	ESTs	other
18335	.3019961487	AA018587	ESTs Weakly	?
33036	.2915644973	W48580	ESTs Weakly	other
30180	.2897721925	N33144	ESTs	SS.
35691	.2895541242	AA401758	ESTs Weakly	?
25340	.2721717135	AA054554	EST	?
28108	.2659103745	AA485084	ESTs	other
38690	.2649184307	AA600121	ESTs	other
20203	.2626499431	N28855	ESTs Modera	other
10251	.2608780694	R76185	ESTs Weakly	SS.
12684	.2604192389	AA417558	ESTs	SS.
31636	.2509469427	N73680	Natural resista	TM
20769	.2479765348	N67277	ESTs	other
1572	.2353281083	K01884	EST - K01884	?
10923	.2292322072	AA116035	ESTs	other
34380	.2283792392	AA252414	ESTs	other
10132	.2222816115	R35733	EST - R35733	other
16629	.2161752119	AA036811	ESTs	?
25146	.1969883794	AA026356	ESTs	?
28730	.1865943098	D20959	ESTs Modera	other
10200	.1874912391	R64521	ESTs	other
38695	.1545794663	AA600176	ESTs	other
31365	4.150549979	N67550	ESTs	other
42379	.1486120688	W37899	ESTs	other
28050	.1428703354	AA479139	Acid phosphat	other
2620	.1386565707	M29474	Human recom	?
8927	.1340593744	AF008442	Homo sapiens	other
13379	.1269549188	AA449741	ESTs Weakly	other
5134	.1218251808	U79293	Human clone	other
2626	4.1213948	M29581	Zinc finger pro	other
38005	.1160483666	AA479969	ESTs	other
36576	.1127196584	AA431085	EST	?
18296	.1121837207	AA213820	ESTs Weakly	?
29531	.1111459313	H88953	EST - RC_HQ	TM
143	.1095880506	AFFX-HUMT	AFFX-HUMT	?
10970	.0967613396	AA129390	ESTs	other
25836	.0952825397	AA152305	Interferon (gam	SS.
19735	.0937927853	H53038	EST	?
40711	.0909709431	N53564	ESTs	other
4149	.0901471427	U28386	RAG (recomb	TM
5767	.0862784557	X53793	MULTIFUNCT	other

FIGURE 12
(cont.)

5503	.0861035825	X05232	Sirometysin	SS,
20310	.0841711656	N34893	ESTs Highly	other
456	.0599824566	D38145	Prostaglandin	SS,
7814	.0559685576	AA248406	ESTs	other
40230	.0447282719	H90161	ESTs	SS,
33651	4.039204804	W95409	ESTs	other
16777	.0231657926	AA046968	EST	?
19110	.0094905222	H08778	ESTs	other
34442	.0077010365	AA258093	HKR-T1	other
5099	4.004992433	U79247	Human clone	TM
6209	.9990473163	AA384220	ESTs	other
24408	.9976586074	W90146	ESTs	other
26596	.9974919787	AA279943	ESTs	other
18485	.9811264006	AA026269	Spleen focus	other
32969	.9804901745	W42451	ESTs	TM
27006	.9799768093	AA398695	ESTs Weakly	other
29809	.9526765967	N21043	EST	?
8596	.9440163451	H91564	ESTs	TM
29024	.9377933936	F09315	Homo sapiens	other
21694	.9356365584	R39317	Homo sapiens	other
13207	3.929998104	AA443321	ESTs	other
37865	.9143752626	AA476623	ESTs Highly	other
38201	.9129828172	AA421164	ESTs	?
8961	.8981160269	AFFX-HUMT	AFFX-HUMT	?
17444	.8927133917	AA115933	ESTs	other
25869	.8919834527	AA157267	ESTs Highly	TM
24862	3.89042252	Z41415	ESTs Highly	other
26685	3.889363206	AA281950	ESTs	?
42300	.8850230366	T95850	ESTs	?
6495	.8830844863	X92715	Zinc finger pro	other
38604	.8828045942	AA598803	ESTs	TM
38358	.8826713716	AA425756	ESTs	other
30560	3.873276445	N49284	MYB PROTO	other
14413	.8724466158	AA600150	ESTs	other
23823	.8574824967	T91805	Homo sapiens	other
38158	3.853096838	AA487021	EST	?
2572	.8518747554	M27281	Vascular endo	other
40100	.8464168967	H75933	Laminin recep	other
40258	.8462992993	H93340	ESTs	TM
20944	.8461821525	N74443	ESTs	other
20411	.8459400966	N48963	Homo sapiens	other
10345	.8457714481	AA001663	ESTs	other
31261	.8451974374	N66248	EST	other
8513	.8378410994	AA446990	ESTs	other
13877	.8363409835	AA476604	ESTs	other
40748	.8253562321	N56879	EST	?
14509	.8152852193	AA609943	ESTs	other
10281	.8065567331	R60333	ESTs	other
25284	.8044158642	AA045074	ESTs Weakly	other
6730	.7900025129	Y09305	H.sapiens mR	other
16033	.7884592402	AFFX-HUMIS	AFFX-HUMIS	?
39242	.7827164808	AA821523	ESTs	other
27354	.7794760439	AA425221	ESTs	?
4552	3.777263605	U49188	Human placen	SS, TM
18385	.7756199108	AA227219	Homo sapiens	other
16754	.7677416053	AA046067	EST - RC AA	other

FIGURE 12
(cont.)

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12752	.7871137403	AA421250	ESTs	other
42463	.7601033106	W60180	ESTs	other
10614	.7581669016	AA037357	ESTs	?
867	.7459337969	D87716	Human mRNA	other
7608	.7336047135	AA180967	ESTs	other
31785	.732738742	N80703	ESTs	other
35377	.7273784603	AA399453	EST - RC_AA	?
22828	.7243928524	R98192	ESTs	other
25240	.7243198336	AA039713	ESTs	other
11008	.7197361356	AA134289	ESTs Weakly	?
4341	.7162349944	U38545	Human ARF-a	other
28833	.7147818393	D59787	EST - RC_D8	?
3750	.7121007154	U09279	Collagen type	SS,
17483	.6943413512	AA122147	ESTs	TM
16854	.691520847	AA055552	ESTs Weakly	TM
3709	.689165677	U07550	Heat shock 10	other
1608	.6852978422	L00205	KERATIN TYP	?
24577	.6617721053	Z38727	Homo sapiens	TM
31032	.6570916386	N62508	ESTs	other
4851	.6536195433	U69546	Human RNA b	other
37680	.6523275307	AA460225	ESTs	other
20418	.649535709	N49209	ESTs	other
27995	.6485167436	AA470155	Homo sapiens	?
7871	.6434397185	AA287423	ESTs	other
27606	.643030453	AA443793	ESTs	other
24677	.6427250633	Z39338	ESTs Highly	other
11070	.6406198277	AA148521	ESTs Weakly	TM
9328	.6356048599	D89518	Homo sapiens	other
36826	.634689802	AA435996	ESTs	other
17678	.6300045795	AA134275	Human HIV1	other
36209	.6274694477	AA421266	ESTs Weakly	other
34120	.6258090412	AA211615	EST	?
38152	.6248442011	AA486737	H.sapiens mR	TM
38463	.6184693268	AA504491	ESTs Weakly	TM
20064	.6183699978	H98653	ESTs	TM
31256	.5992620732	N68152	EST	?
9713	.5985228843	L44338	Homo sapiens	other
28622	.5768056147	D11837	ESTs	?
38057	.5736105703	AA481549	EST - RC_AA	other
28763	.5688723791	D45568	EST	?
16996	.5680705709	AA069038	EST - RC_AA	TM
28628	.5604144817	D11886	ESTs Modera	?
25804	.5442954572	AA148885	ESTs	?
2492	.5423964239	M22898	Tumor protein	?
14904	.5411970737	T83389	ESTs Highly	other
25265	.5347588502	AA043765	H.sapiens RY	other
13608	.5327912417	AA458437	ESTs Weakly	other
42307	.5318436465	T96595	EST - RC_T96	TM
1544	.526232414	J05068	TRANSCORBA	SS,

FIGURE 12
(cont.)

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Accession	Gene	Score	Accession	Gene	Score	Accession	Gene	Score	Accession	Gene	Score
CZAR	111928	3.7	R40057	promitin (mouse)-like 1							
BCX2	128780	4.0	AA291725	secreted frizzled-related protein 4							
CBC2	101809	5.7	A183849	Homo sapiens connexin 26 (Cx26) mRNA, complete cds							
CBC1	100365	4.5	D78111	mesoderm specific transcript (mouse) homolog							
CBC3	102610	2.5	U65932	extracellular matrix protein 1							
	134804	6.3	L37036	small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)							
	104208	2.1	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated							
CJA8	115697	8.1	AA411502	ESTs: Weakly similar to airway trypsin-like protease [H.sapiens]							
	124315	5.4	H94892	v-r1 simian leukemia viral oncogene homolog A (ras related)							
	109415	4.3	AA272719	Homo sapiens CAGF9 mRNA; partial cds							
	103613	5.1	Z46629	SRY (sex-determining region Y)-box 9 (campomelic dysplasia; autosomal sex-reversal)							
	109166	6.2	AA179845	RAB6 Interacting; kinesin-like (ropkinstin6)							
CJA9	115176	5.7	AA63725	ESTs: Weakly similar to KIAA0726 [H.sapiens]							
CGA7	115522	8.1	AA331303	ESTs							
	125852	5.7	H05290	ESTs: Weakly similar to unknown [H.sapiens]							
BCN5	112244	3.1	R51303	ESTs							
COA1	132592	5.6	AA129390	ESTs							
BCN7	117280	5.4	N72107	ESTs: Moderately similar to [H] ALU SUBFAMILY SC WARNING ENTRY [H] [H.sapiens]							
	102663	4.8	U70322	karyopherin (importin) beta 2							
COA2	104680	6.0	AA007160	ESTs							
	113702	2.4	T87307	ESTs: Moderately similar to [H] ALU SUBFAMILY J WARNING ENTRY [H] [H.sapiens]							
	100154	6.0	D14657	KIAA0101 gene product							
	102260	3.7	U28386	Human nuclear localization sequence receptor hSRPalpha mRNA, complete cds							
	101809	5.7	M66849	Homo sapiens connexin 26 (Cx26) mRNA, complete cds							
	133272	3.2	AA465016	ESTs: Highly similar to serine protease homolog							
	100365	4.8	D78111	mesoderm specific transcript (mouse) homolog							
	128819	4.7	AA305536	EST176522 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence							
	132543	4.6	AA417152	ESTs: Highly similar to protein regulating cytokinesis 1 [H.sapiens]							
	103023	5.5	X53793	multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase							
	132109	3.1	AA590801	ESTs							
	104037	3.5	AA372630	differentially expressed in hematopoietic lineages							
	104978	3.5	AA080458	ESTs: Weakly similar to [H] ALU SUBFAMILY J WARNING ENTRY [H] [H.sapiens]							
	108995	3.0	AA121316	ESTs							
	107248	3.8	D58894	ESTs							
	132902	3.4	AA490969	ESTs							
	120104	4.0	W95477	ESTs							
	128790	4.0	AA291725	secreted frizzled-related protein 4							
	101923	3.2	S75256	HNL-neutrophil lipocalin [human, ovarian cancer cell line OCE, mRNA Partial, 534 nt]							
	119943	3.4	W86835	copine III							
	130648	3.9	AA076427	ESTs							
	132358	3.5	X00486	H4 histone family, member G							
	100286	3.2	AA434441	frizzled (Drosophila) homolog 7							
	117557	2.3	N33920	disubiquitin							
	129601	3.3	X06700	collagen, type III; alpha 1 (Ehlers-Danlos syndrome type IV; autosomal dominant)							
	114767	4.5	AA148985	minichromosome maintenance deficient (S. cerevisiae) 4							
	100335	3.8	D63391	platelet-activating factor acetylhydrolase; isoform II; gamma subunit (29kD)							
	134989	3.5	AA298324	ESTs: Weakly similar to [H] ALU CLASS A WARNING ENTRY [H] [H.sapiens]							
	110009	3.4	I110933	ESTs							
	124059	4.0	F13673	ESTs							
	104755	2.2	AA024482	ESTs: Weakly similar to epidermal type I keratin [H.sapiens]							
	107151	3.4	AA621169	ESTs							
	132969	2.9	AA188378	ESTs: Weakly similar to 60S RIBOSOMAL PROTEIN L22 [H.sapiens];							
	104394	5.5	H40617	yp19h1.1 Soares breast 3NoHst Homo sapiens cDNA clone (IMAGE:187821 5', mRNA sequence							
	117667	2.5	N39214	src-Thr protein kinase relates to the myotonic dystrophy protein kinase							
	104934	3.3	AA074514	ESTs: Moderately similar to (define not available 4753768) [H.sapiens]							
	132994	3.7	AA505133	ESTs							
	102881	3.7	U72781	karyopherin (importin) beta 3							
	103989	2.2	AA314779	ESTs: Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]							
	132103	2.5	L19183	Human MAC30 mRNA; 3' end							

FIGURE 13A

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118685	3.0	N71781	ESTs	
100552	3.4	HG2167-HT22Protein Kinase H31, Camp-Dependent		
120471	2.5	AA251820	ESTs; Moderately similar to (define not available 4680597) [H.sapiens]	
126547	4.2	U47737	transmembrane 4 superfamily member 3	
106557	3.3	AA417007	ESTs	
125103	4.0	T95333	ESTs; Weakly similar to Strabismus [D.melanogaster]	
135243	3.4	AA215333	ESTs	
121457	2.5	AA411446	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	
131218	2.7	C31058	ESTs	
112971	2.4	T17185	ESTs	
111179	2.1	N67239	ESTs	
123533	2.3	AA608751	ESTs; Moderately similar to [H] ALU SUBFAMILY SC WARNING ENTRY [H] [H.sapiens]	
105175	2.4	AA186004	ESTs; Weakly similar to unknown [S.cerevisiae]	
105156	2.7	AA172372	ESTs; Moderately similar to [H] ALU SUBFAMILY SQ WARNING ENTRY [H] [H.sapiens]	
111223	2.5	N68921	ESTs; Weakly similar to neogenin [H.sapiens]	
132180	2.7	AA405559	fibroblast activation protein; alpha	
105400	2.1	AA447621	ESTs	
125260	3.1	AA093834	ESTs; Highly similar to (define not available 4679014) [H.sapiens]	
115291	3.9	AA279943	ESTs	
128828	2.1	C14037	ESTs; Weakly similar to Yel007c-ap [S.cerevisiae]	
116399	2.7	AA599720	Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds	
130987	3.5	R45698	ESTs	
105082	2.6	AA143763	ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C.elegans]	
103453	3.2	X09585	H.sapiens mRNA for SMT3B protein	
115947	2.6	AA443783	ESTs	
105012	2.8	AA116036	ESTs; Highly similar to (define not available 4589929) [H.sapiens]	
105507	3.2	AA256878	ESTs; Moderately similar to (define not available 4108051) [H.sapiens]	
130800	2.6	AA223386	ESTs; Weakly similar to katanin p80 subunit [H.sapiens]	
116461	3.4	AA621557	ESTs; Moderately similar to [H] ALU SUBFAMILY SQ WARNING ENTRY [H] [H.sapiens]	
129945	2.5	AA232104	ESTs; Highly similar to (define not available 4929579) [H.sapiens]	
100864	2.1	HQ4297-HT45Transcriptional Coactivator Pca		
128131	2.3	A1283182	claudin 3	
131564	2.8	AA481465	ESTs	
100278	3.1	D42084	Human mRNA for KIAA0094 gene; partial cds	
134425	1.8	J04177	collagen; type XI; alpha 1	
130287	2.6	AA113149	tumor suppressing subtransferable candidate 3	
108828	2.1	AA131584	ESTs; Weakly similar to coded for by C. elegans cDNA cm16f6 [C.elegans]	
131289	2.2	AA485697	ESTs	
109141	4.2	AA176428	ESTs	
119307	2.5	T32108	ESTs	
134319	2.1	AA129547	ESTs; Moderately similar to [H] ALU SUBFAMILY J WARNING ENTRY [H] [H.sapiens]	
133458	5.0	M18728	non-specific cross reacting antigen	
116732	2.3	F13779	ESTs; Weakly similar to [H] ALU SUBFAMILY J WARNING ENTRY [H] [H.sapiens]	
CGAB	115239	3.0	AA278650	ESTs

FIGURE 13B

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Code	PRIMEKEY	Accession	Complete Title
CZA8	111929	3.7	R40057 prominin (mouse)-like 1
BCX2	128790	4.0	AA291725 secreted frizzled-related protein 4
CBC2	101809	5.7	M86849 Homo sapiens connexin 26 (GJB2) mRNA, complete cds
CBC1	100365	4.6	D78611 mesoderm specific transcript (mouse) homolog
CBC3	102618	2.5	U65932 extracellular matrix protein 1
CJA8	115697	8.1	AA411502 ESTs: Weakly similar to airway trypsin-like protease [H.sapiens]
CJA9	116176	5.7	AA463725 ESTs: Weakly similar to KIAA0226 [H.sapiens]
CGA7	115522	8.1	AA331393 ESTs
BCN5	112244	3.1	R51309 ESTs (now Sulfatase by in-house sequencing)
CQA1	132592	5.6	AA126390 ESTs
BCN7	117280	5.4	N22107 ESTs: Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]
CQA2	104660	6.0	AA007160 ESTs

FIGURE 14

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FIGURE 15

ATGACCATGATTACGCCAAGCTTGGCAGGAGGAGACAGCCACTTGGCCATGTCACCAAAACAAGGAGAAGGTGCAAGAC
TGTCCGTGTGGACCTGACTCACAGCAGAATCATTGAGAGATAAAATAAGTAATCCCCTGAATCCAGAATCATGAAA
AGCAGGAAAGCCAGGATCTCAGAGCTACTGCAAAAGTTCTTCTCCACUAGACGAGCACCAGAAGCTGAGAATGCTGTT
TCCTCAGGTAACAGAGATTCAAGGTACCTTCAGAAGGAAAGAAATCTCTACACAGATGAGTCATCCAAACCTGGAAA
AATAAAAGAACTGCAATCACTACTCCAAACTTTAAGAAGCTTCATGAAGTCAATTTAAGGAAATGGAGTCCATTGATC
AATATATTGAGAGAAAAAGAAACATTTTGAAGAACACAATTCATGAATGAAGTGAAGCAGCAGCCCATCAATAAGGGA
GGGETCAGGACTCCAGTACCTCCAAGAGGAAAGACTCTCTGTGGCTTCTACTCCCATCAGCCAACGACGCTCGCAAGGCCG
GTCTTGTGGCCCTGCAAGTCAGAGTACCTTGGGTCTGAAGGGTCACTCAAGCGCTCTGCTATCTCTGAGCTAAAACGG
GTGTCAGGTTTTTCAGCTGCTACTAAAGATAATGAGCATAAGCGTTCCTGACCAAGACTCCAGCCAGAAAGTCTGCACAT
GTGACCGTGTCTGGGGCACCCAAAAGGGCAGGGCTGTGCTTGGGACACACAAATTAAAGACCATCACGGGGAATTCTGC
TGCTGTTATTACCCCATTTCAAGTTGACAACTGAGGCAACGAGACTCCAGTCTCCAATAAGAAACCAAGTGTGATCTTA
AAGCAAGTTTGTCTCGTCCCTCAACTATGAACCAACAAGGAAAGCTAAAACCATGGGGGCAATCTAAAGAAATAAT
TATCTAAATCAACATGTCAACAGAATTAAGTTCTACAAGAAAACCTTACAACAACCCCATCTCCAGACAAAGGAAGAGCA
ACGGAAGAAACGCGAGCAAGAACGAAAGGAGAAGAAAGCAAAGGTTTTGGGAATGCGAAGGGGCTCATTTTGGCTGAAG
ATTA

FIGURE 16

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MTMITPSLARGROPLGHVTKTRRRCKTVRVDPDSQCNHSEIKISNFTFONHEKQESQDLRATAKVSPPPDEHQEAENAV
SSGNRDSKVPSEGGKSLYDESSKPGKNKRTAITTPNFKKLHÉAHFKEMESIDQYIERKKKHFEHNSMNELKQQPINKG
GVRTPVPPRGRLSVASTPISQRRSQGRSCGPASQSTLGLKGLKRSASAAKTGVRFSAAKDNHEKRS�TKTPARKSAH
VTVSGGTQKGEAVLGTHLKTITGNSAAVITPFKLTTEATQTPVSNKKPVFOLKASLSRPLNYEPHKGKLPWGQSKENN
YLNQHVNRINFYKKTYKQPHLQTKKEQKKREQERKEKKAKVLGMRRGLILAED

FIGURE 17

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Amino-CKVLG MRRGL ILAED-COOH

FIGURE 18

Acetyl-KQPHL QTKEE QRKKC-Amide

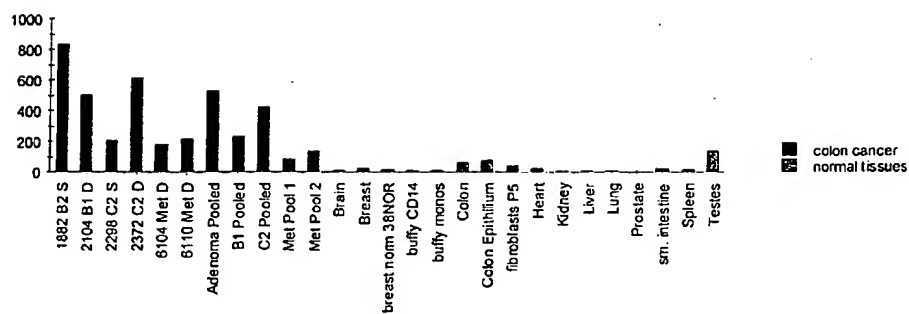
FIGURE 19

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human_CAA2 -----KKHFEFHNSMNELKQPINKGGVRTVPVPPGRLSVASTFISQRRS
mouse_CAA2 AREKKMESIDENIMRKKKHLKEHSSLNEIKLUKK--GIVTPVPFGRLSVPCTPARQQCP
          .....*..... : * : .....*..... :
human_CAA2 QGRSCGPASQSTLGLKGSILKRSASAAKTGVRFSAATKDNEHKSLTKTPARKSAHVTVS
mouse_CAA2 QG-----H--S-ATKMNVRFSAATKDNEHKSLTKTPARKSPHVTAP
          .. : ..* : .....*..... :
human_CAA2 GGTQKGEAVLGTHKLKITGNSAAVITPFKLTTEATQTFVSNKKPVFDLKASLSRPLNVE
mouse_CAA2 GSASKGOAVERTPKSKATERTSIAVITPFKLMTEATQTPSSSKKPVFDLKASLSRPLNYK
          .....*..... : .....*..... :
human_CAA2 PHKGKILKPWGQSKENNYLNQHVNRIIFYKITYKOPHLQTKEEQKKKREQERKEKKAKVLG
mouse_CAA2 PHKGKILKPWGOAKENNSLNERVSRVTFHRKITYKOPHLQTRERWKRQEQERKEKKKELLE
          .....*..... : .....*..... :
human_CAA2 MRRGLILAED-
mouse_CAA2 ARRNLGVTKAQ
          **.* :

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FIGURE 20

**FIGURE 21**

GGTGGCCTCTGTGGCCGCTCCAGCTAGCGGCGCGCCGACGAGCGCGGGAGAAAGACTCTCTACCTTGGTCTTGGCGGCTTG
TGGGCACCGCCCGGCGGGGCTGTGGAGGGCCGTGCTCCGGGAGAGCTCCCGCGGCTCTGCACTTCCGCGCGGGGCTCGGGC
AGCTATTGAGCGCCCGGCGGCTAGCGGGCTCTCTCCGGGCGCGGAGCTCGCGGGGTCCGGGGAGACCGGCTCAGCCGCTGT
CGCTGGCCGCGACGAGGTTGGAACCTCCGCGGACGGTGTGGCCCTCGGTCGCGGAGGATGCTCGGCCCGCGAGCCGCGGAGC
GGCGCGGGGTCCGCGATGAGGGCCCGCGCGCGCGGGGACGAGGCTGGGACAGCCCTTGGGGCCACCCCTGACGACGAG
CGCTTTTCAGGTGGAAGCTGTGTTTTCGAGAGAACGGGCGCGGCTGCTGTCCGGCGCGGGTCCGGGGCGGCGCGCGCGG
CGGCTGTGGTCTTGGGCGGGGGCCAAAGCAGACGCCCGCGGAGCGGGGAAAGCCAGCGGCGAGAGCGAGCCAGCTAAAGGCGAGC
GAGGAAGCCAAAGCGCCCTTCCGCGGTAACTTCTGGAACCTCGCTCCGCTCGGTGGAAGCAGCGCTGTTCAGATGTC
TGCCGGGGTCCGAGTGCAGCGGGCCAACTGTGAGCTTCCAGAAAGCGGGGACACGGTGTGAGCGAGGGGACGAGCAGCTCT
ACTCGCGGCGGGGCGGAGCTGGGACGAGTGGGACCAACGAGCAGCTACTATGATACCAACCAACCTCACTGCTCGGCACC
TTCCGCGCAACAAACCTGAGACGTGTGCCACAGATGCATACCTACCGGCACACGCGCGAGCTGGGCGAGAAGCTGTC
CCGGCCTAGCTTGGCGAGCTCCACGACGAGCTGGAAAAGGAACCTTTTGAAGATGGCTTTGCAAAATGGGGAGAAAGATA
CTCCACACAGAGATGCTGTGGTGCAGTATCTAGCGAGAAAGTAAAGGAGCTGTAAGTTGGCTGCGTGATAGAGGTTGTA
GTACGTGTATGTATTAACATTTGGGGTGATGTATGCTTTTCAATAGTATGTCAATGTTGGTCGAGTCAAGTGAAGATGCTT
ATCAGTCTCTGTATAATGATGGCCACTGTTGTGACAACTATCACAGGATTTGTCTACTTTCAGCAATAGCAACTAATGAT
TGTTAAGAGAGGAGGAGGACGATTTTAAATATCTAGAAGTCTAGGSGCGAGAAATTTGGTGGTGCAATTTGGTCTTAATCTTC
GGCTTTGCCAAGCTGTGCAATTTGCTATGTATGTGTGGATTTGCAAGAAACGCTGGTGAGAGTGCTTAAGGAACATTC
CATACTTATGATAGATGAATCAATGATATCCGAATTAATGGAGCCATTACAGTCGTGATTTCTTTAGGTATCTCAGTAG
CTGGAATGAGGTGGGAAGCAAAAGCTCAGATTTGTTCTTTGGTGATCTTACTTTCTGATTTGGTGATTTTCGTACATGGA
ACATTTATCCCACTGGAGAGCAAGAAGCAAAAGGGTTTGTGTTATAAATCGAAATTTAATGAGAACTTTGGGCC
CGATTTTCGAGAGGAAGAGACTTTCTTTTCTGTATTTGCCACTTTTTCCTGCTGCAACTGGTATTTGGCTGGAGCAA
ATATCTCAGGTGATCTTGGCAGATCTCTCAGTCAAGCTACCCAAAGGAACCTCTACCGATTTTAAATACTACTATGTGTT
TAGCTAGGAATTCAGATATCTGTAGGTTCTTGTGTTTGCAGATGCACTGGAAAGCTTAATGACACTATCGTAACAGA
GCTAACAACTGTACTTCTCGAGCCTGCAAAATTAACCTTTGATTTTTCATCTTGTGAAGCAGTCTTGTGTTCTATGGCC
TAATGACAACTCTCCAGGTTAATGAGTATGGTGTGAGGATTTACACCACTAATTTTTCGAGGATATTTTTCGACCACTCT
TTCTTCAGCATTAGCATCTCTAGTGTAGTGCTCCCAAAATTTTCAGBCTCTATGTAAAGGACAACTACCCAGCACTTCCA
GATGTTTGCTAAAGGTTATGGGAAAAATATGAACCTCTCTGTGGCTACATCTTAACATCTTAATTTGCACCTTGGATTCA
TCTTAATTTGCTGAACGTGAATTTATTCGACCAATTTCTCAAACTTTCTTCTGTCATATGATATGATCAATTTTTC
GTTATTCATGCTCACTTGCAGAAATCTCCAGGATCGGGCTCTGCAATCAALATACCAACATGATGATATCACTCTTTGG
AGCAATCTTTGTTGTCATAGTAATGTTCCGTCACTAATCTGGTGGCTGCACTGTCATACATATGTGATAGTCTTTGGGCTGT
ATATTTTCTTACTTCAACAAAAACAGATGTGAATTTGGGAGCTCTCTACACAAGCCCTGACTTACTCGTATGCATCGAGC
CAITTCATTTGCTCTTTTCGGATGGAAGACAGGATGGAAGAAACTTTAGGCCACAGTGTCTTGTATGACAGGTGCTCCAAA
CTCAGCTCGAGCTTTACTTTCATCTTGTATGATTTACAAAAAATGTTGTTTGTATGATCTGTGGCCAGTGTACATATGG
GCTCTCGAAGACCAAGCCATGAAGAGATGCTCCATCGATGCAAGCCAAATACAGCGAGTGGCTTATTAAGAACAAATGAAG
GTATTTATGCTCCAGTACATGCAGATGACTTGAAGAGAGTGCAGATGATTTGATGCGAGCTGTGGTCTTGTGCTGAT
GAAGCCAAACAGCACTTGTCTTGGATTTAAGAAAGATTTGGTTCGACAGCAGATAGAGGAGGTGTGATATGATATAAACT
TATTTCAATGATGCTTTTGACATCAAAATGGAGTAGTGGTTATTTCGCTTAAAAAGAGGTCTGGATATATCTCATCTCAA
GGACAAGAAAGATTTATGTCATCAAGAGAAATCTCTGGACCAAGAGTGGTGTAGTAAGTGTGGAATATAGTAAAGAA
GTCCGATTTAGATATCTCCAAAGCTCAGTGAAGAAACCAATACACACAAAGTTGAGGAAGAGGATGCAAGACGTCAA
CTCAACCACTGTGAAAAAGAAATCCAAAGGCCCTATTGTGCTTTAAATGTAGCTGACCAAAAGCTTCTTGAAGCTAGT
ACACAGTTTCAGAAAAAACAAGAAAGAAATATTTAGTGTCTGGTGCTTTTGTATGTAGGAGTTTGAACCTTATTTGAT
ACCTTACCTTCTGACGACCAAGAAAAAATGGAAGAGCTATGAAGTACAGATATTCATGTGGGAAGATAAAGCAAGATAG
ACCATAGCCGAGAGAGCTGTGCTACTTTGCTTAGCAAGTTCCGGATGCACTTTTCTGATATCATGTTCTAGAGATATC
AATACCAAAACCAAGAAAGAAATATTATAGCTTTTGGAGGAATCATTTAGGCCATACAGACTTCATGAAGATGATAAAGA
CGAAGATATTGCGATATAAAATGAAGAGATGAACCTGCGGAATAACAGATATAGTCTGAACTTATGAAGACCAAGA
CATACCGGACAGTACAGTTTAAATGAGTTATTAAGAGAACTTCAAGCAGCTAATATTTGTGATGAGTCTCCCACT
GCACGAAAAAGGTGCTGTGTCTAGTGCTCTACATGGCATGGTTAGAAGCTCTATCTAAGGACCTACCCCAATCTCTCT
AGTTCTGGTGAAGATCATCAGAGGTGCTCTTCACTTCTATGAAATGTTCTATACAGTGGACAGCCCTCCAGAAATGGTACT
TCAGTGGTGTGATGTAGTAACCTGAAATCTTCAATGACACTAATACATCAAGTGGCAATGTGATGACTTTTCTTCAAGAT
TTCATTAATTTGAAGACACACAGGAAGGCTTGCTCATTGATAACGTGTATGGAGACTTCGGTTTTAGTCAATCCCATAT
CTCAACTTAAATGGTGATTTCTCTCTGTGAACTGAAGTTTGTGAGAGTAGTTTCTCTTGTCTACTTGAATAGCAATAAA
ACGGTGTTAACTTTTGG

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ATGAGAGCCGCGCCACACGGCGCCCTCTCTCGGCGCCCGGGACTGCGCGGGGTCGGGGAGACGCGGTACGCCGTGCGCT
GGCCGACAGCCAG33TGGAACTCGCCCGGCAC3GCTGTGCCCTCGGGTCGCGGAGATGCTGCGCCCGACGCGCGGACCGCG
TTCGGGCTCCGACCTGAGGACGCCCGCGCGCGCGGACGGGCTGGGACAGCCCTTGGGGCCACCCCGACGACGAGCGCT
GTCCAGGTGCGACT3GTTTCCGAGAGCGCGCGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGGACGCGCGCGCG
TGGTGCTGGGCGCGCGGCCAAGCAGACCCCCGCGGACGGGAAGCCAGCGCGAGAGCGAGCCAGCTAAAGGCGACGAGS
AGCAAGCAAGGCGCGCTTCCGCGTGAACTTGTGCGAGCCAGCTGCCCTCTGCTCGGCTGAAGACAGCTGTCAGATGTGCC
GGGTGCGGAGTGCAGCGGCCCAAGCTGAGCTTCCAGAACCGCGGGACACGCTGCTGAGCGAGGGCAGCAGCTGCACCTC
CGCGCGCGCGCGCGCGCAGTGGGCACCAACAGCAGCTACTATTATGATACCCACACCAACCTACTACTGCTGCCACTCTCG
CCCAACAACTGAGCTGAGCGCTGTGCCAGGATCGATCACTACTCCGACACAGCGCGCAGCTGGGCGAGAAGCTGCTCGC
CTAGCTCTGGCGSAGCTCCACAGCGAGCTGGAAAAGGAACCTTTTGAAGATGGCTTTGCAAAATGGGGAAGAAAGTACTCC
AACCAGAGATGCTGTGGTCACGTATATCTGCAGAAAGTAAAGGAGTCGTGAAGTTGCTGGCTGGATCAAGAGGTGTATTAGTAT
GTTGCTGTGTAACAACTTTGGGGTGATGTGCTTTTCACTTAGTTGTGTCATGGATTGTGGGTCAGCTGGAAATAGGCTCTATCA
GTGCTGTGTAATAATGATGSGCACTGTGTGACAACTATACAGGATGTCTTACTTCAGCAATAGCAACTAATGGATTGTGT
AAGAGGAGGAGGAGCATATTTATTAATATCTAGAAGCTTAGGGCCAGAATTTGGTGTGTGCAATTTGGTCTAATCTTCGCCCT
TTGCGCAACGCTGTTGTCAGTTGCTATATGTATGGTTGGATTTCGACAAACCGTGTGGAGTTGCTTAAGGAACATCTCAT
CTTATGATAGATGTAATCAATGATATCCGAATTATTGGAGCCATACAGCTGCTGATTTCTTAGGTATCTCAGTAGCTGG
AATGGAGTGGGAAGCAAAAGCTCAGATTGTTCTTTTGGTGTATCTACTTCTTGCTATTGGTGATTTTCGTCATAGGAACAT
TTTCCCTCAGTGAGAGCAAGAAAGCAAAAGGGTTTGTGGTTATAAACTGMAAATTTAATGAGAAGCTTTGGGCGCGAT
TTTCGAGGAGGAAGAGACTTTCTTTCTGTATTGGCATCTTTTTCTGCTGCAACTGGTATTCTGGGTGGAGCAAAATAT
CTCAGGTGATCTTGCAGATCTCTCAGTCAGCCATACCCAAAGGAACACTCCTAGGCCATTTAAATCTACATAGTTGGTTTACG
TAGGAATTTGTCAGTATCTGTAGGTTCTGTGTTGTGTCAGATGCCACTGGAAACGTTAATGACATCTGTAACAGAGCTA
ACAAACCTGTACTCTGCGAGCTGCAAAATAAACTTTGAGATTTCATCTGTGAAGCAGCTGCTTGTTCCTATGGCCCTAAT
GAACAACCTTCCAGCTAATGAGTATGGTGTCAAGGATTACCAACCACTAATTTCTCGAGGTATATTTTCGCCACCTCTTTCTT
CAGCATTAGACTCCCTTAGTGAGTGTCTCCCAAAATATTTACAGGCTCTATGTAAAGCAACACTTACCAGCTTTCCAGAT
TTTGCTAAAGGTTTAGGGAATAAATGAACCTCTCTGGGCTACATCTTAACCTTTAATGTGCACTTGGATTCATCTT
AATGTCTGAACTGAATGTTATTGCAACCAATTATCTCAAACCTCTCTCTGTCATATGACATGATCAATTTTTCAGTAT
TCCATGTCATCACTTGTCAAAATCTCCAGGATGGCGCTCTGCTCAATTAACATACAACATGTGGATCACTCTTCTGGAGCA
ATCTTTTGTGTCAGATAGATTGTTGCTCACTTAACATGTTGGGCTGCACTGTCTAACATATGTGATAGTCTTTGGGCTGTATAT
TTATGTTACCTACAAAAAACAGATGTGAATTTGGGATCTCTACACAAGCCCTGACATAGCTGAAAGCAGCTGACAGCAT
CAATTCGCTCTTCTGAGTGGGAAGCAGCTGAAAAAATTTAGGCCACAGTGCTTGTATTGACAGGTCGCTCCAAACTCA
CGTTCCGCTTTTACTTCGATCTTGTGTCATGATTTTCAAAAAATGTGGTTTGAATGATCTGTGGCCATGTACATATGGGTCC
TCGAAGACAAGCCATGAAGAGAGATGCCATCGATCAAGCCAAATATCAGCGATGGCTTATTAGAACAATAAGGAGCAT
TTTATGCTCCGATCATGTCAGATGAGCTGTGAGAGAAGGTGCAAGTATTGATGTCAGGCTGCTGGTCTTGGTGTATGAAG
CAAAACACCTTGTCTCGGATTTAAGAAAGATGTTGTTCGAAGCAGATATGAGGATGGTGATATGTATATAAACTTATT
TCATGATGCTTTTGACATACAATATGGAGTAGTGGTTATTTCGCTCAAAGAAAGGTTCTGGATATATCTCATCTTCAAGGAC
AAGAAGAAATATTATGTCATCAAGAGAATACTCTCGCAACAGGATGTGGTAGTAAGTGTGGAATATAGTAAAGATCCG
GATTTAGATACTTCAAAACCTCAGTGAAGAAACCTATACACAAGAGTGAGGAGAGAGATGGCAAGACTGCAACTCA
ACCACCTGTTGAAAAAAGAAATCCAAAGGCCCTATTGTGCGCTTAAATGTAGCTGACCAAAAGGCTTCTGAAGCTGATACAC
AGTTTTCAGAAAAAACAGGAAGAAATATATAGCTTGTGATGCTGGTGGCTTTTGAATGATGAGGATTTTAACTTATGATCACT
TACCTTCTGACGACAGAAAGAAATGGAAGAGCTGTAAGATACAGATTAATCACTGGTGGAAAGATACAGAATAGACCA
TGACCGGAGAGCGATGGCTACTTTGCTTAGCAAGTTCGGGATAGACTTTCTGATATCATGGTCTTAGGAGATATCAATA
CCAAACCAAGATAAGAAATATATATAGCTTTTGAAGAAATCATTTGAGGCCATACAGACTCATGAGATGATAAAGAGCAA
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CCGCGAGATCAGGTTAAATGAGTTATTAAGGAACCTTCAAGCAGAGCTAATATTATTGTGATGAGTCTCCCAAGTTGCAC
GAAAGAGTGCTGTGTTCTAGTGTCTCTCATATGCGCATGGTTAGAAGAGCTCTATCTAAGGACCTACCACCAATCTCTTAGTT
CGTGGGAATCATCAGAGTGGCTCTTACTCTTATTCAZAA

MEPRPTAPSSGAPGLAGVGETPSAAALAAARVELPGTAVPSVPEDAAPASRDGGGVRDEGPAAAGDGLGRPLGPTPSOSR
FQVDLVSENAGRAAAAAAAAAAAGAGAGAKOTPADGEASGESEPAKGSSEAKGRFRVNFVDPAASSSAEDSLSDAA
GVGVDPNVSPONGGDTVISESSSLHSGGGGSGHHOHYYDTHNTYLRFTGHNTMDAVPRIDHYRHTAAQLGEKLLR
PSLAELHDELEKEPFEDGFANGEESTPTRDAVVITYAESKGVVKFGWIKGVLVRCMLNIWGYMLFIRLSHIVGOAGIGLS
VLVIMMATVYTTITGLSTSAIATNGFVRGGGAYYLSRSLGPEFGGAIGLIFAFANAVAVAMYVVGFAETVVVELLKEHSI
LMIDEINDIRIIGAITVVILLQISVAGMEWEAKAOIVLLVILLLAIGDFVIGTFIPLSKKPKGFFGYKSEIFNENFGPD
FREEETFFSVFAIFFPAATGILAGANISGDLADPQSAIPKGTLLALLITTLVYVGIAYSVGSCVVRDATGNVNDTIVTEL
TNCTSAACKLNFDPFSSCESSPCSYGLMNNFQVMSMVSGFTPLISAGIFSATLSSALASLVSA PKI FOALCKDNIYPAFQM
FAKGYGKNNEPLRGYILTFILALGFIILAEINVIAPILISNFFLASVALINFSVFHASLAKSPGWRPAFKYNNMISLIGA
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PNTLVLGFKKDWLQADMRDVMYINLFHDAFDIQYGVVIRLKEGLDISHLOQEELSSQEKSPGTDVVVSVEYSKKS
DLDTSKPLSEKPIHKVEEEDGKTATQPLLKESKGPVPLNVADQKLEASTQPKKQGGKTIDVWWLFDDGGLTLLIP
YLLTTKKKWKDCKIRVFIGGKINRIDHRRAMATLLSKFRIDFSIMVLGDINTKPKKENTIAFEEIIEPYRLHEDDKEQ
DIADKMKEDPWRITDNELELYKTKTYRQIRLNELLKEHSSSTANIIVMSLPVARKGAVSSALYMAWLEALSKDLFPILLV
RGNHQSVLTFYS

FIGURE 24

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FIGURE 25

Peptide names	Solubility	
CAA9p1	1mg/1ml H2O	H-CDPAASSSAEDSLSD-NH2
CAA9p2	1mg/1ml H2O	Ac-KKSDLDTSKPLSEKC-NH2
CAA9p3	1mg/1ml H2O	Ac-PLKKESKGPVPLC-NH2
CAA9p4	min.amt.DMSO/H2O	Ac-EHSILMIDEIC-NH2
CAA9p4MAPS	1mg/ml buffer pH7.5	Ac-EHSILMIDEIC-on 8-Branch Maps
CAA9p5	1mg/1ml H2O	Ac-DFREEETC-NH2
CAA9p5MAPS	1mg/1ml H2O	Ac-DFREEETC-on 8-Branch Maps

GGCACGAGGAGAAGCTTAAAGAAATTCAGATATGTGAAGTTGATTTCCAGGAAACCTCGTCA
 TCTCTGATGACAGTTGTGACAGCTTTGCTTCTGATAATTTTGCACACAGGCGTGCAGTCA
 GTTCGGGAAAGGCTGTAGGACCCGACGCCATGCAAGGCATCTGGACCTCTCAGGTCGGCAT
 GAAGTTTCCAGCGCGGATGACCGAGGCAACCAAAAAAGCAGATCCGCCGACGCCCT
 CAGAGAAATCTGTGACTGATTCCAATCCGATTCAAGAAGTGAAGTGAATTTTTTTGG
 AGAAAAAGGGCTTTAAATAATAAGAGAAAAACAAGCAATGCTTGCAAAATCTGTGTAATTA
 GAAAGCTTCCCTGGCTGCTTGGTGAAGACATCCCTCCCGAGCTCGCATCAAACTCAAGG
 AGACCGCGAAGGGCTACATTTCCCGGGTGTGTGCTTCAGAGGAAACCCCTGACCGGAGGCTCG
 TCCTCTTACAGGCTCAAGTCCCGGATCTCCGGGTCTCCAGCTTACCGATACCCAATAATTCGC
 CGATTGAAGAAATAAGTACAGGAGGAGGTGGAGAACGCTTCAGCAATTCGCAAGAGA
 ACAGTTAAACCGTTTCACTGGGTTCTATTGTCTCAATAGCCGTGAGAAGACTATTGATACCA
 AACAAATCGCAAAACCCAGACTCTGGGCGCTTCGAGGCCAGTTCTGTGGCCCTGCTCCCTTG
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 TATATTGTCTAGTACACTTGTGCCCTCGAGTTCTTCTCTGCCACCCCCATCTCATAGC
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 AAWTTACAGTTTAAAGGAAAAAGCATATTTATTTACCTGGGTGTGGAAATAGGCCCTCCAT
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 GAGAAGAGCCTTCTAACTTGTTTACAAAAAACAGGATGATTTAGCATTCATACAGTTGATCA
 ATTITTTAATAGAAATCAAGGCCACAAAAGTTCTAAAAACCATGTGGAATAATAGGTAATTTATKGA
 ARATTGAKGTTGTCYCYCAATCCCAAGYGAATKSSGTTATGKTACMARKKGKTGTGCMCAGTTAG
 ACYTAATTTTCYCTTAATTTCTCTCYGSCGAAGGKWAAGKGGKGGCTCCRGCTACMCGATCAT
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 AGATTAWGAGTGAAGCTGATTGAAATTTTCAGATTTATAAACTTTAGTATAATTGTATGTTGCAAA
 GKTTATTTCAGTTCACATGTAAGGKATTTGCMATAATTTCTTGGACAAATTTTGKATGGAACCT
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 GTTCAAGTTTATGATTTTAAAGCATTTTATAACAATGATAAGTGCCCTTTTGGAGATGTAACCTT
 TAGCAGTTTGTAAACCTGACATCTCTGCCAGTTGATTTCTGGGACGAGTTCTCTGTGTCAGTAT
 TCCCGCTCTCTTTGATATTAATCAAGGATTTTGTAGAGGTGGAATCAAGTTTGTGATGTC
 CAATTTATCTTGATATGTAAACCATTTGCTGTGCCATTCAATGCTTTTATACAAAAGTTTATT
 CTGTAATCGATAAGTGTAAATACAGCTTTTGATCTGTAATGCTTTTATACAAAAGTTTATT
 TTAATAATAAAATGTTTGTCTTAAAAAATAAATAAATAAATAAATGCGGCGCAGAGCTTATT
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 CACTTGCACGCGCCTAGCGCCGCTCTTTCGCTTCTTCTCTCTCTCTGCMGCTTCCGCGG
 CTTTTCGCCCAAGCTNTAAATCGGGG

One position equals 20 bases
 ■ if more than 2 bases disagree with consensus sequence's
 ■ if more than 10 positions are unknown
 ■ if more than 10 positions are gap characters

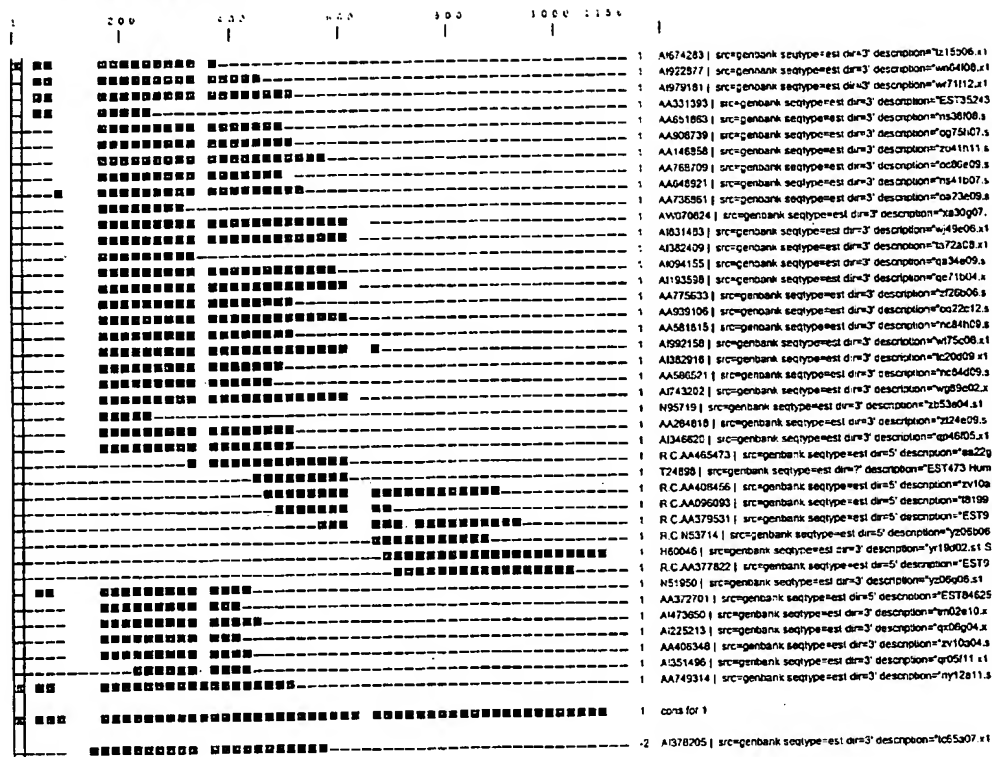


FIGURE 28A

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AA585521 | srcgenbank seqtype=est dir=3 description="nc84d09.x1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:787489 3', mRNA 5' src=gbes11648294
AD43202 | srcgenbank seqtype=est dir=3 description="w35e02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:237 src=gbes118434
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FIGURE 28B

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ARSTRGATNK KAESRQPSN SVTDNSDSE DESGMNELEK RALNIQNKA
MLAKLMSELE SFPQSFRGRH PLPGSDSQSR RFRRTFPGV ASRRNPERRA
RPLTRSRRI LGSIDLALPME EEEEEKYML VRKRTVDGY MNEDDLPRTR
RYRSSVTLPH IIRPVVEIQK ERSWRTSAAI LEEKIITVHW ALLVINAVRR
LLIPKQTAET QTAGAFEASS VAPAFETVMV KRSGMLCWIR TGIARLVEES
ATAVSAGSEM RGVRLGSLCI

FIGURE 29

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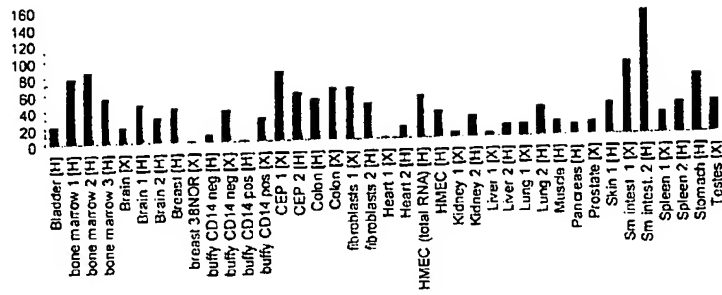


FIGURE 30A

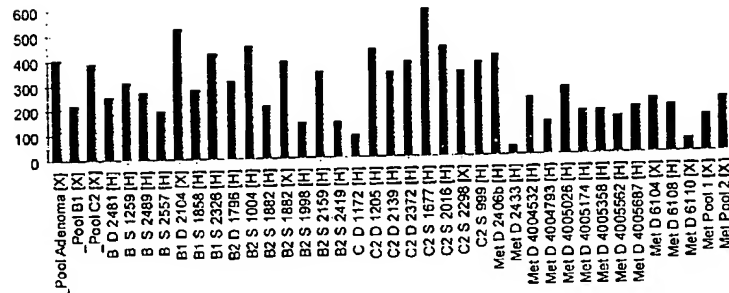


FIGURE 30B

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ACTCACTATNGGGCGAATGGGCCCTCTNNATGCATGCTCGAGCGCCCGCCAGTGTGATGGATA
TCTGCAGAAATTCGCCCTTAAGCAGTGGTAACAACGCAGAGTACGCGGGGGGAGACCGGAGGG
CAGAAGGCAGAGTCCAGGCTTAGACTGCAGTTCCTCGCTTACCTGTGCAGTCTAATTTTGAGC
TGCCCTTTTGTAGTCTTAAAGGCAGGAGCTTCGTGTTGTGGGTCTGCTAACCCGTACGTTTCC
GTGGGCAAGTCGTGTGTACTCCTCGCCCTGCTCAGCTCCAAACACGCTTCTACACTGATAAC
AAGAAATATGCCGTAGATGATGTTCCCTTCTCAATCCCTGCTGCCTCTGAAATGGCCGACCTTA
GTAACATCATCAATAAACTACTAAAGGACAAAAATGAGTTCACAAACATGTGGAGTTTGATT
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AGTGCTTCTATGGATCAGACTATTCTTATGGGAGTGGAAATGTAGAGAGAAACAAAGTGAA
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TAAATGGTCTCCTACCATGAACAGCAGCTGATTTCAGGATCTTTAGATAACATTGTTAAGC
TGTGGGATACAAAGATTGTAAGGCTCCTCTCTATGATCTGGCTGCTCATGAAGACAAAGTTC
TGAGTGTAGACTGGACAGACAGGGCTACTTCTGAGTGGAGGAGCAGACAATAAATTGTAT
TCCTACAGATATTACCTACCACTTCCCATGTTGGGGCACTAAGTGAACAATAATTGACTA
TAGAGATTATTTCTGTAATGAAATTTGGTAGAGAACCATGAAATTACATAGATGCAGATGCA
GAAAGCAGCCTTTGAAGTTTATATAATGTTTACCCCTTCATAACAGCTAACGTATCACTTT
TTCTTATTTGTATTATAAATAGATAGGTTGTGTTTATAAAATACAACTGTGGCATACA
TTCTCTATACAACTTGAAATTAACCTGAGTTTACATTTCTCTTTAAARGTAAAAA
AAAAA

FIGURE 31

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170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 115
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FIGURE 32A

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AA807828(11) | srcgenbank seqtype=est dir=3 description="hu90c09.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1217990 3' mRNA" srcgbest1976988
AA219575(11) | srcgenbank seqtype=est dir=3 description="x03c05.s1 Striatone NT2 neuronal precursor 637230 Homo sapiens cDNA clone IMAGE:1122843
AA278650(15) | srcgenbank seqtype=est dir=3 description="ts78a08.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:703870 3' mRNA s" srcgbest24145
AJ076659(17) | srcgenbank seqtype=est dir=3 description="cc08g04.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:2544493 3' siml" srcgbest234586
AW058555(17) | srcgenbank seqtype=est dir=3 description="wv23d07.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2544493 3' siml" srcgbest3551329
AI126947(10) | srcgenbank seqtype=est dir=3 description="cb96a12.x1 Soares_fetal_heart_Nb-H18W Homo sapiens cDNA clone IMAGE:1707" srcgbest2350375
AA173577(10) | srcgenbank seqtype=est dir=3 description="z004807.s1 Striatone ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:1048663
AJ766182(18) | srcgenbank seqtype=est dir=3 description="wh70n03.s1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2368143 3' siml" srcgbest332826
AA084295(18) | srcgenbank seqtype=est dir=3 description="am15a06.s1 Soares_NFL_T_GDC_S1 Homo sapiens cDNA clone IMAGE:1466668 3' " srcgbest2063489
AA912878(19) | srcgenbank seqtype=est dir=3 description="cd27b02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524651 3' " srcgbest215252
AW104628(20) | srcgenbank seqtype=est dir=3 description="x084c08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604303 3' " srcgbest36072
AA932938(21) | srcgenbank seqtype=est dir=3 description="0006g02.s1 Soares_NFL_T_GDC_S1 Homo sapiens cDNA clone IMAGE:1565426 3' " srcgbest128801
AJ082380(21) | srcgenbank seqtype=est dir=3 description="ta70h07.x1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:20" srcgbest256831
AJ278377(21) | srcgenbank seqtype=est dir=3 description="qm63e06.x1 Soares_placenta_8dweeks_2NbHPBc9W Homo sapiens cDNA clone IMAGE:12538348
AB17342(23) | srcgenbank seqtype=est dir=3 description="wv22d07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2413044 3' siml" srcgbest3517498
AA903844(23) | srcgenbank seqtype=est dir=3 description="ak64e11.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518784 3' siml" srcgbest216261
AF073354(24) | srcgenbank seqtype=est dir=3 description="wv25a08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2291854 3' siml" srcgbest317760
AZ462255(24) | srcgenbank seqtype=est dir=3 description="qu39c01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1587136 3' siml" srcgbest256231
AF096102(24) | srcgenbank seqtype=est dir=3 description="t03d10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239898 3' mRNA s" srcgbest3190525
AA911053(24) | srcgenbank seqtype=est dir=3 description="ak65e03.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518844 3' siml" srcgbest217487
AF080131(24) | srcgenbank seqtype=est dir=3 description="wv65b10.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2254539 3' siml" srcgbest3114554
AF052510(24) | srcgenbank seqtype=est dir=3 description="wv67g10.x1 NCI_CGAP_B18 Homo sapiens cDNA clone IMAGE:2548770 3' siml" srcgbest3729164
AF052510(24) | srcgenbank seqtype=est dir=3 description="wv74g05.x1 NCI_CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549432 3' mRNA" srcgbest3721327
AF170999(24) | srcgenbank seqtype=est dir=3 description="q78g12.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:2114950 3' siml" srcgbest3723775
AA502237(26) | srcgenbank seqtype=est dir=3 description="he26a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:898444 3' mRNA se" srcgbest1546530
AA907840(32) | srcgenbank seqtype=est dir=3 description="om18c08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541198 3' " srcgbest214257
AA528399(102) | srcgenbank seqtype=est dir=7 description="hnd0g12.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910918 mRNA seque" srcgbest1574499

cont for 1

FIGURE 32B

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MAQLQTRFYTDNKKYAVDDVPFSIPAASELADLSNIINKLLKDKNEFHKHVEFDF
 LIKGQFLRMPLDKHMEMENISSEEVVEIEYVEKYTAPQPEQCMFHDDWISSIKGA
 EEWLTGSYDKTSRIWSLEGKSIMTVGHTDVVKDVAWVKKDSLSCLLLSASMD
 QTILLWEWNVERNKV KALHCCRGHAGSVDSIAVDGSGTKFCSGSWDKMLKIWS
 TVPTDEEDEMEESTNRPRKKQKTEQLGLTRTPIVTLSGHMEAVSSVLWSDAEEIC
 SASWDHTIRVWVVEGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHRLWDPR
 TKDGSLSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDTRSCAPLYDL
 AAHEDKVLSDWDTGTLLSGGADNKLYSYRYSPTTSHVGA.

FIGURE 33

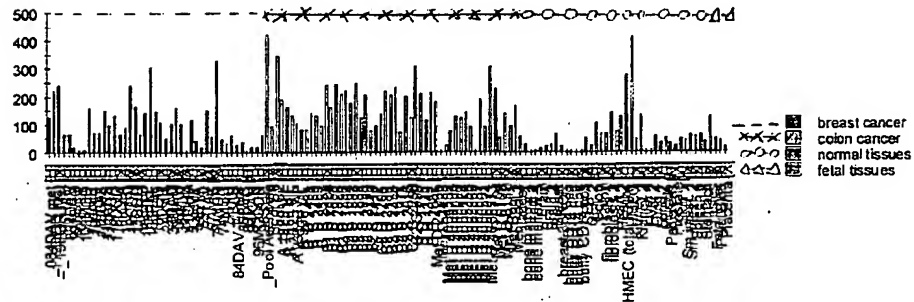


FIGURE 34

FIGURE 35

FIGURE 36

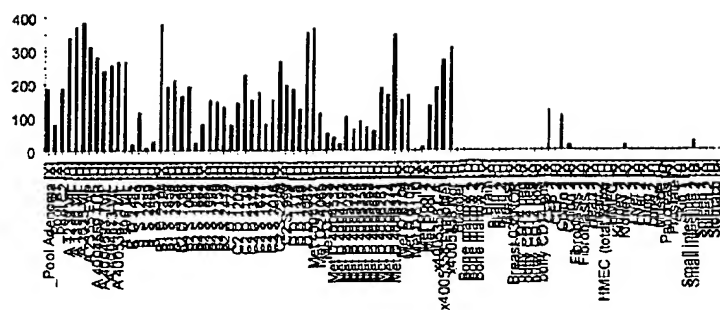


Figure 37

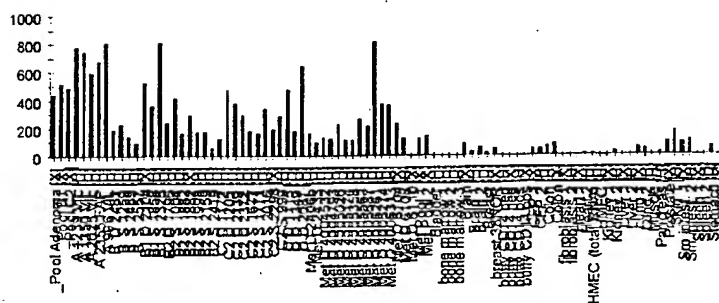


Figure 38

AGAATCGCTTCGGCTCCITTCGCCGCCGGTATCTSSIGTATATGATCCCACTCTCACTCTCATAGGAGAC
GATCTCGAAGTAGATCATATACACCAAGATACCGGCCGCGAAGGAGCCGAAGCTCAAGGGTAAAGACAGTA
GAAATATTATTCAGTAAACAATAATGTGTGAACCTTTAAGATGGATAATAGGGCATGGACTGAGTGCTGCT
ATCTTGAAATGTGCACAGGTACACTTACCTTTTTTTTTTTTTTTTTTAAGCTTTCCCAITCAGGATAACA
ACATIGTGATCTGTACTACAGGAACCAATGTCAATCCGTATACATGTGGCTATAAAGTACAT/AAATATA
TCTAATCTATTCAT/ATGTGGGGTGGGTAATACTGTCTGTGAATAATGT/AGAAGCTTTTCACTTAAAAAA
AATGCAITTACTTTCACTTAACTAGACACCGGTGGA/AAATTTCAAGGTTATAGTACTTATTCAACAA
TTCTTAGAGATGCTAGCTAGTGTGGAAGCTAAAAATAGCTTTATTTATGCTGNAATTGTGATTTTTTATGC
CAAAATTTTTTAGTTCTAATCATTTGATGATASCTTGG/ATAAATAATTATGCCATGGCATTTGACAGTT
CATTTATTCCTATAA/AAATAAATTGAGTTTAGAGAGAATGGTCGTGTGAGCTGATTATTAACAGTTACTG
A/ATCAAAATATTTATTTGTACATTATTCATTTGTATTTTAGCTTTCCCTTTACATTTCTTTATATGCA
TTCTGACATTACATATTTTTAAGACTATGGA/AAATAATTAAGATTTAAGCTCTGGTGGATGATTATCTG
CTAAGTAAGTCTGAAAAATGTANTATTTGAC/AAATACCTGTAATATACCTGTACACAAATGCTTTTCTAATG
TTTTAACCTTGAGTATTCCAGTTGCTGCTTTGACAGAGGTTACTGCAATAAAGGAAGTGGATTCAATTAA
CCTAAAAA

FIGURE 39

CCAAGTTCTACCTCATGTTTGGAGGATCTTGCTAGCTATGGCCCTCGTACTCGGCTCCCTGTTGCTGCTGG
GGCTGTGCGGGMACTCCTTTTCAGGAGGGCAGCCCTTCATCCACAGATGCTCCTAAGGCTTGGAAATTATGAA
TTGCCGTGCAACAAATATGAGACCCAGACTCCCATAAAGCTGGACCCATTGGCATTCTCTTTGAAGTAGT
GATATATCTTTCTCTATGTGGTACAGCCGCGTGATTTCCAGAAAGTACTTTGAGAAAATCTTTACAGAAGG
CATATGAAATCCAAAATGATTATGACAAAGCCAGAACTGTAACTCTAGGTCTAAAGATTGTCTACTATGAA
GCAGGGATTATCTATCTGTGCTCGTGGGCTGCTGTTTATTATTCTGATGCTCTGGTGGGGTATTTCCTT
TTGTATGTGCTGCTGTGCTGTAACAAATGTGGTGGAGAAATGCACAGCGACAGAAAGAAATGGGCCCTTCC
TGAGGAAATGCTTTGCAATCTCCCTGTTGGTGATTGTATATAATAAGCATTGGCATCTTCTATGTTTTT
GTGGCAATCACCAGGTAAAGAACCCGGATCAAAAGGAGTCGGAAACTGGCAGATAGCAATTTCAAGGACTT
GCGAACTCTCTTGAAATGAACTCCAGAGCAATCAAAATATATATGGCCCACTACACACTACCAAGGACT
AGCGCTTCACAGATCTGAACAGTATCAATTCAGTGCTAGGAGGCGGAATTTCTGACCCAGTACAGACCAAC
ATCATCCCTGTTCTTGATGAGATTAAAGTCCATGGCAACAGCGATCAAGGAGACCAAGAGGCGTTGGAGAA
CATGAACAGCACCTTGAAGAGCTTGACCAACAAAGTACACAGCTTAGCAGCAGTCTGACCAAGCTGAAAT
CTAGCCTCGGTCATCTCTCAATGACCTCTGTGCTTGGTGATCCATCAAGTGAACCTGCAACAGCATC
AGATTGTCTTAAAGCCAGCTGAATAGCAACCTGAACTGAGGCGAGCTTCCACCCGTTGGATGCAGAACTTGA
CAACGTTAAATACGTTCTTAGGACAGATTGGATGGCTGGTCCACAGGGCTATCAATCCCTTAATGATA
TACCTGACAGAGTACACCCCAACACAGACTGTGCTAGCAGGTATCAAAAGGGCTTGAATTCCTTGGT
TGAGATATCGAATGTAATCAGCGCTCTCTTATTGAGGATATCTCTCAGCATCTCTGTTTATGTTAA
TAACTCTGAAAGTTACATCCACAGAAATTTACCTACATTGGAAGAGTATGATTCACTGTTGGCTGGGTG
GGCTGGTCTATGCTCTCTGCTGACCTCTCATCGTGAATTTTACTACCTGGGCTTACTGTGTGGCGTGGC
GGCTATGACAGGCATGCCACCCGACCCAGCGGCTGTGTCTCCACACCCGAGGCGCTCTCTCTATGTT
TGGAGTTGGATTAAAGTTTCTCTTTTGGTGATATTGATGATCAATGTGGTCTTACCTTTGTCTTTGGTG
CAATGTGGAAAAGCTGATCTGTGAACCTTACACAGGCAAGGAATTTATCCCGGTTTGGATACACCTAC
TTACTTAATGAAAGCTGGGAATACTATCTCTCTGGGAAGCTATTTAATAAATCAAAATGAAGCTCACTTT
TGAAAGATTACAGTGACTGCAAAAAAATAGAGGCACTTACGGCACTCTTCACTGCAGAACAGCTTCA
ATATCAGTGATCTCAACATTAAATGAGCATACGGAAGCATAAGCAGTGAATGGAAAGCTGAAGGTA
AACTTAATATCTTTCTGTTGGGTGACGAGGAAGAAACCTTACAGGATTTGCTGCTTGTGGAAATAGA
CAAGATGAATTAATGACAGCTACTTGGCTCAGACTGGTAAATCCCCCGAGGAGTGAATCTTTTATCATTTG
CATATGATCTAGAGCAAAAGCAACAGTTTGGCCCGAGAAATTTGAGGAATCCCTGAAAGAGATGCA
CAAACTATTAAACAAATTCACAGCAACGAGTCTTCTATAGAACAATCACTGAGCACTCTATACCAAG
CGTCAAGATACTTCAACGCACAGGGAATGGATTGTTGGAGAGATTAAGGATTCTAGCTTCTCTGGATT
TTGCTCAGAACTTCAACCAAACTACTTCTCTGTTATTATTAGGAAACTAAGAGATATGGGAGAAC
ATAATAGGATATTTTGAACATTATCTGCAAGTGGATCGAGTTCTCTATCAGTGAGAAAGTGGCATCGTGCA
ACCTGTGGCCACCGCTCTAGATACTGCTGTTGATGCTTTCTGTGTAGCTACATTATGACCCCTTGAAT
TGTTTTGGTTGGCATAGGAAAGCTACTGTAATTTTACTTCCGGCTCTAATTTTGGCGTAAACTGGCT
AAGTACTATCGTCAATGGATTGCGAGGACGTTGACGATGATGTTGAACTATACCCATGAAATATGGA
AAATGGTAAATAGGTTATCAAAAGATCATGTATATGGTATTCACAATCCCTGTTATGACAGCCCATC
AACATTCATAGCTGATGTTGAAACTGCTTGAACATCAGGATACCTCAAGTGGAAAGGATCACAGATTTTG
GTAGTTTCTGGGTCTACAAGGACTTCCAAATCCAGGAGCAACGCGAGTGGCAACGTAGTGACTCAGGCG
GCACCAAGGCAACGCGACCATTTGGTCTCTGGGTAGTGCTTAAAGATGAACCAATCACGTTATAGTCCAT
GGTCCATCACTATTCAAGGATGACTCCCTCCCTTCTGCTATTTTGTGTTTACTTTTACACTGAGT
TTCTATTAGACACTACACATATGGGGTGTGTTGCCATGGATGCAATTTCTATCAAACTCTATCNA
TGATGAGGCTGATTTTCAACATATGCCATGTGTGGAGTGTGCTGAACACACACAGGTTTACAGGAAGAT
GCATTTTGTGTACAGTAACCGGTGTATATACCTTTTGTACCACAGAGTTTTTAAACAAATGAGTATTAT
AGGACTTTCTTAAATGAGCTAAATAAGTCAACATTGACTTCTGGTGCTGTTGAAATTAATCAATTTT
ACTAAAGTGTGTAAACCTACAGCATATTTCTACGCAAGAGATTTTCTATCTATATCTTTATCAAGAT
TGGCCATCTTCACTTGGAAATGGCATGCAAAAGCCATCATAGAGAACTGCGTAACCTCATCTGACNA
TTCAAAAGAGAGAGAGATCTTGAGAGAGAAATGCTGTTCTGTTCAAAAGTGGAGTTGTTTAAACAGATGC
CAATACCGGTGTACGTTTAAACAGGTTTCTGTGCTAGGATTAACATTAATTTGAGTGCAGCTAACA
TGAGTATCATCAGACTAGTATCAAGTGTCTAAATGAATATGAGAAGATCCTGTCAAACTCTTAGATC
TGGTGTCCAGCATGGATGAAACCTTTGAGTTTGGTCCCTAAATTTGCATGAAGACACAGGTAATATTCA
TTTGTCTCAGGAGTTTCTATGTTGGATCTGTCAATATCAAAAGTATCAGCAATGAAGAACTGGTGGACAA
AATTTAAGCTGTATGTAATGAAATCCAGATGTAGGCATTTCCCGCAGGTCTTTTATGTGAGATTCAG
TTCTGATTCATTGAATAAAAGGAACCTCG

FIGURE 40

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CAGCGGCGCTGAATTCAGGGCGGGTTCGGCGCCCGAAGGCTGAGAGCTGGCGCTGCTCGCTGCCCTGTG
TGCAGACGGCGGAGCTCCGCGGCCGACCCCGCGGCCCGCTTTGCTGCCGACTGGAGTTTGGGGGAAG
AAACTCTCTCGCGCCAGAGATTTCTTCCTCGGCGAAGGACAGCGAAAGATGAGGGTGGCAGGAAGA
GAAGGGCGCTTTCTGTCTGCCGGGTCGACGCGGAGAGGGCAGTGCCATGTTCTCTCCATCCTAGTGGC
GCTGTGCCCTGTGGCTGCACCTGGCGCTGGCGGTGCCGCGCGCGCCCTGGAGGGCGGTGCCATCCCTATG
TGC CGGCACATGCCCTGGAACATCACCGGATGCCCAACCACCTGCACACAGCAGCGAGGAGAACGCCA
TCTTGGCCATCGAGCAGTACGAGGAGCTGGTGGACGTGAACCTGCAGCGCGCTGCTGCGCTCTTCTTCTG
TGCCATGTACGCCCATTTGCACCTGGAGTTCTTGCAGACCCCTATCAGCCGTGCAAGTCCGTGTG
CAACGCGCGCGGACGACTGCGAGCCCTCATGAAGATGTACAACACAGCTGGCCCGAAAGCCTGGCCT
GCGACGAGCTGCTGTCTATGACCGTGGCTGTGCATTTGCGCTGAAGCCATCGTACGGACCTCCCGGA
GGATGTTAAGTGGATGACATCACACAGACATGATGTTACAGGAAGGCTCTTGATGTTGACTGTAA
CGCTAAGCCCGATCGGTSCAAGTGTAAAAAGGTGAAGCCACTTTGCCAAGTATCTCAGCAAAACT
ACAGCTATGTTATTATGCCAATATAAAGCTGTGACAGGAGTGGTGCATGAGGTGACACCGGTGGT
GGATGTAAAGAGATCTTCAAGTCTCATCACCCATCCCTCGAAGTCAAGTCCCGCTCATACAAATCT
TCTTGGCAGTGTCCACACATCTGCCCATCAAGATGTTCTCATCATGTTACGAGTGGCGTTCAAGGA
TGATGCTTCTTGAAATGTCTTAGTTGAAAAATGGAGAGATCAGCTTAGTAAAGATCCATACAGTGGGA
AGAGAGCGCTGCAGGAACAGCGGAGAACAGTTTCCAGGACAGGAAGAACAGCGCGGCGCACCACTCGTAGT
AATCCCCCAAAACCAAGGGAAAGCCTCCTGCTCCCAACCAGCCAGTCCCAAGAGAACATTAATACTA
GGAGTGGCCAGAGAGAACAAACCCGAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAGACTTCCGAC
TTCCCTTACAGGATGAGGCTGGGCTTGGCTTGGTACAGAGGTGAGTTAAGCTGAGTTAAGCTGGTGA
ACTCACTGCAGTGTCTTATAGACACATCTTGCAGCATTTTCTTAAAGGCTATGCTTCACTTTTCTTT
CTAAGCCATCACAAGCCATAGTGGTAGTTTGGCTTGGTACAGAGGTGAGTTAAGCTGGTGGAAAA
GGCTTATTCATTGCAATCAGAGTAACCTGTGTGATCTCTAGAGAGTGGGAAATATGCTTGTGA
CAATTCGACCTAATATGTGCAATGTAAATTAATGCCATATTTCAAACAAACAGTAATTTTACAG
TATGTTTTATTACCTTTTGATATCTGTTGTTGCAATGTTAGTGTGTTTTAAATGTGATGAATATAA
TGTTTTTAAGAGGAACAGTAGTGGAAATGTAATTAAGATCTTATGTGTTATGGTCTGCAGAGGA
TTTTTGTGATGAAAGGGGTTTTTTGAAAAATTAGAGAAGTAGCAATGGAATTAATATGTTTTTT
TACCAATGACTTCAGTTTCTGTTTTTAGCTAGAACTTAAAAACAAATATAATTAAGAAAAATTAAT
AAAGAGGAGGAGCAGACATGTCTGGATTCTGTTTTTGGTTACCTGATTTCCATGATCATGATGCTTC
TTGTCAACACCCCTTTAAGCAGCACCAGAACAGTGASTTTGTCTGTACCATTAGGAGTAGGTACTAAT
TAGTTGGCTAATGCTCAAGTATTTATACCCACAGAGAGGTATGTCACTCATCTACTTCCAGGACAT
CCACCTGAGATAATTTGACAGCTTAATAAGGCTTCAATGTGAGTGGCAATTTTGTGTTTTCTTCAT
TTAAATATTTCTTTGCCTAATAACATGTGAGAGGAGTTAATATAAATGTACAGAGGAAAGTTGAGT
TCCACCTCTGAATGAGAATTACTTGACAGTTGGGATACTTTAATCAGAAAAAAGAACTTATTTGCAGC
ATTTTATCACAATTTTATATTTGTGGACAAATGGAGGCATTTATTTAAAAAACAAATTTTATTGGCCT
TTTGTAAACAGTAAGCATGTATTTTAAAGGCATTCATAAATGCACACGCCCAAGGAATAAAT
CCTATCTATCCTACTCTCACTACACAGAGGTATCACTATTAGTATTTGGCATATTTCTCCAGGT
GTTTGCCTATGCCTTATAAATGATTTGAACAAATAAACTAGGAACCTGTATACATGTGTTTCATAAC
CTGCCCTCTTGTCTGGCCCTTATTTAGATAAGTTTCTCTGTCAAGAAAGCAGAAACCTCTCATTCT
AACAGCTGTGTTATATTCATAGTATGCTTACTCAACAACTGTGTGCTATTGATACTTAGGTGGT
TCTTCACTGACAATACTGAATAAATCATCTCACCGAATTC

FIGURE 41

GAATTAATCCTATGACAACTAAGTGGTTCCTCTCACCTGTTTGGTGAGGTGTGTAAGAGTTGGT
GTTTGGCTCAGGAAGAGATTAAGCATGCTTGCTTACCCGACTCAGAGAAGTCTCCCTGTTCTGTCCTAG
CTATGTTCCCTGTTGTTGTGCTTCGTCTTTCCAGAGCAACCCGCCAGAGTAGAAGTGGATTGGGGC
ACGCTGCAGACGATCCTGGGGCGTGTGAACAAACACTCCACCAGCATTGGAAAGATCTGGCTCACCGTCC
TCTTCATTTTTCGCTATATGATCCTCGTGTGGCTGCAAGGAGGTGTGGGAGATGAGCAGGCGGACTT
TGTCTGCAACACCCCTGCAGCCAGGCTGCCAAGACGTGTGCTACGATCACTACTTCCCATCTCCACATC
CGGCTATCGGGCCCTGCAGCTGATCTTCTGTCTCAGCCAGCGCTCCTAGTGCCCATGCACGTGGCTACC
GGAGACATGAGAGAAGAGGAAGTTCATCAAGGGGGAGATAAAGAGTGAATTAAGGACATCGAGGAGAT
CAAAACCCAGAACCTCCGCTCGAAGGCTCCCTGTGGTGGACCTACACAAGCAGCATCTTCTCCGGGTG
ATCTTCGAAGCCGCTTCATGTACGCTCTCTATGTCTATGTACGACGCTTCTCCATGCAGCGGCTGGTGA
AGTGCACGCTGCGCTGGCTTGTCCCAACACTGTGGACTGCTTGTGTCCCGGCCACGGAGAAGACTGCTT
CACAGTGTTCATGATTGCAGTGTCTGGAATTTGCATCCTGCTGAATGTCACTGAATTTGTATTATTGCTA
ATTAGATATTGTTCTGGGAAGTCMAAAAGCCAGTTTAAAGCATTGCCAGTTGTAGATTAAAGAAATAG
ACAGCATGAGAGGGGATGAGGCAACCCGCTGCTCAGCTGTCTAGGCTCAGTCCGCAAGCATTTCCCAACACA
AGATTCTGACCTTAAATGCAACCATTTGAAACCCCTGTAGGCTCAGGTGAACCTCCAGATGCCACAATG
AGCTCTGCTCCCTAAAGCCTCAAAACAAAGGCTAAATCTATGCTGTCTTAAATTTCTTTCACTTAAG
TTAGTTCCTCTGAGACCCAGGCTGTTAGGGGTTATTGGTGTAAAGTACTTTCATATTTAAACAGAGGA
TATCGGCATTGTTCTTTCTCTGAGGACAAGAGAAAGCCAGGTTCCACAGAGGACA/CAGAGAAGGT
TTGGGTGTCTCTCGGGGTTCTTTTGCCAACTTCCCCACGTTAAAGGTGAACATTGGTCTCTTCAATTT
GCTTTGGAGTTTAAATCTCTAACAGTGGACAAAGTTACAGTGGCTTAAACTCTGTACACTTTTGGGA
AGTGAAACATTGTAGTATGATAGGTTATTTGTATGTAAAGATGTTCTGGATACCATTATATGTTCCCCC
TGTTTCAGAGGCTCAGATTGTAAATGTAAATGTATGTCTATCGCTACTATGATTAAATTTGAAATATG
GTCTTTTGGTTATGAATACTTTGCGACACAGCTGAGAGAGGCTGTCTGTTGTATTCATTGTGGTCAATG
ACCTAACACATTGTAGCCTCAATCGAGTGAGACAGACTAGAAGTTCCTAGTTGGCTTATGATAGCAAT
GGCCTCATGTCAAAATATTAGATGTAAATTTGTGTAAAGAAATACAGACTGGATGTACCACCAACTACTACC
TGTAATGACAGGCTGTCCAACACATCTCCCTTTTCCATGCTGTGGTAGCCAGCATCGGAAGAACGCTG
ATTTAAAGAGGTGAGCTTGGGAATTTTATTGACACAGTACCATTTAATGGGGAGACAAATGGGGCCA
GGGGAGGGAGAAGTTCTGTCTGTTAAACAGAGTTTGGAAAGACTGGACTCTAAATTCGTTGATTAAAG
ATGACCTTTGTCTACCTTCAAAAGTTTGTGTGGCTTACCCCTTACGCTCCAATTTTAAAGTGAAT
ATAACTAATAACATGTGAAGAATAGAGCTAAGGTTTAGATAAATATTGAGCAGATCTATAGGAAGAT
TGAACCTGAATATTGCCATTATGCTTACATGGTTTCCAAAAATGGTACTCCACATACTTCAGTGAGGG
TAGATATTTCCTGTTGTCAAGAATAGCATTGTAAAGCATTTTGTAAATAAAGAAATAGCTTTATGA
TAGCTGTAACTAAATTAATTTGTAAATGTATCAATACATTTAAACATTAAATATAATCTCTATAA
T

FIGURE 42

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CGGCCAGCACACCCCGGCACCTCCTCTGCGGGCAGCTGCGCCTCGCAAGCGCAGTGCCGACGCGCACGCCG
GAGTGGCTGTAGCTGCTCGGCGCGGCTGCGGCTGCGGCGGCTGTGGGCTGCGGCTGCGGCTGCGGCTGCGGCT
GCTGCGCAGCTCTGACCGCTGCGGCTGCTGCGGCGGCTGCTGCTGCAACGCTGCGGCGGCGGCGCATG
GCATACCGGCGGCTGCTGCGGCGGCTGCTGCGGCGGCTGCTGCGGCGGCTGCTGCGGCGGCTGCTGCGGCGGCT
CTGGGCTGCGGCT
GCT
TGGAGTCCAGAGATAGTGTGCTTTACACGCTTTCCACATCCAGCTACGACTGCTACAGATTGTTGG
AAGCGCTGACCTTGAGGTTTCATCGGCTGATTGCTTCTTAGGCTTTGGCTTCAGTGACAAAC
CCAGAACCGCAGAAATCAACCTTCTTCTCATGACTATGGAGATATTGTTGCTCAGGAGCTTCTACAGG
TACAGGAGAAATCGATCTGGTGGGATACCAATAAGAGTCTCTGTCTGCTMAATGGAGGTATCTTCTCAGG
AGACTCACCGTCCACTCCTTCTCCAAAGCTACTCAAGATGGAGGTTGCTGCTCAGGCTATCTTCTCAGG
ACTGATGAATCTTCTTGTATTTCTCTCGAGGTCTCACCCGCTCTTGGGCGGTATCTCAGGCTCTGAG
AGTACATCAATCAGAGGAAGAGTTTCAAGAGCGCTGGTGGGAGCTTCTGCTCTGTAATATCCCAT
TCATTTTATCTATGGGCAATTGGATCCTGTAAATCCCTATCCAGAGTTTGGAGCTGTACAGGAAACG
CTGCGCGGCTCCACAGTGTGATTTCTGGATGACCACTTACCACTATCCAGAGTATAGAGGATCCCATGG
GCTTCTTGAATGCATATATGGGCTTCACTCACTCCTTCTGAGCTGGAGAGTAGCTTCCCTGTATTACC
TCCCTACTCCTTATGTGTGTGATTTCCACTTAGGAGAAATGCCAAAAGAGGCTTCCGCGCATCAA
CAATATCTCTCACAAAGTCCACTTTACTCAATTGGTGAACAGTGTATAGGAGAGCCAGCAGGAGCT
CTGACTAAGGTTGACATAATAGTCCACCTCCACTTATGATATCTGATCAAAATGTATAGACTTGGCTT
TGTTTTGTGCTATTAGGAAATTTCTGATGAGCATTACTATTCACTGATGCAGAAAGAGCTTCTTTGCA
TAAAGAGCTTTTTTAAACCTTTGGACTTCTCTGAATATTTAGAGTGTAAATTTCTGCGCCACCCCG
AACAGGAATTTCTATAGTAAAGGAGGAGAGAGGGGGCTCCTTCCCTCTCTCGAATGAGCTTATGGCA
CATGCCTTTTAAAGTCTTTAAGCAACACAGAGCTGAGTCTCTTGTCTATACCTTTGGATTATGTGT
TCATCAGCTGTTTTAGTTATTAACATTTTGTAAATAGATATTGGTTAAATGATACAGTATTTAGG
TATGATTAAGACTATGATTACCTATACATTATATATATTTATAAGATCTAATACCAAGCATACCTT
ACTCTGCCAGAGTAGTGAAGCTAATTAAACACGTTTGGTTCTGAATAAATGAACATAAATCCAACTAT
TTCTTAAATCACAGGACATTAAAGACCAATAGCATCTGTGCCAGAGATGTACITGTTATTAGCTGGGAAG
ACCAATTTCAACAGCAAAATACAGTCTGAGACTCCTCATACCTCAGTGGTTAGAAGCATGTCTCTTTGA
GCTACAGTAGAGGGGAGGGGATTGTTGTGTAGTCAAGTCAACATGCTGATGTACACTGATTCTTTATG
ATGACTGCTTAACTCCCACTGCTGTCCAGAGAGGCTTCCAAATGAGTCTCAGTAATTCCTGTACTT
TACAGACAGGAAAGTCCAGAACTTTAAGAACAACTCTGAAGACCTATGAGCAAAATGGTCTGAATA
CTTTTTTTTAAAGCCACATTTTCTTGTCTTAGTCAAGCAGGATTATTAAGTATTATTTAAATTCGT
TTTTTAAATTAGCAACTTCAAGTATAACAACCTTTGAACCTGGAATAAGTGTATTTCTATTATAAA
AATGAATGTGACAAANAAAAACCG

FIGURE 43

CTCTCAGTGTCCAGTGGTCAGTTGCCCCAGGATGGGGACCACAGCCAGAGCAGCCCTGGTCTTGACCTAT
TTGGCTGTTCGCTTCGCTGCCTCTGAGGGAGGCTTCACGGCTACAGGACAGAGGCAGCTGAGGCCAGAGC
ACTTTCAGAAGITGGCTACGCAGCTCCCCCTCCCCACCCCTATCCCGAAGCCTCCCCATGGATCAGCC
TGACTCTCTCAGCATGGCCCTCCCTTTGAGGGACAGAGTCAAGTGCAGCCCTCCCTCTCAGSAGGCC
ACCCCTCTCCAAACAGGAAAGCTGCTACCTGCCAACTCCCTGCTGAAAGGAAGTGGGTCCCCCTCTCC
CTCAGGAAGCTGTCCCCCTCCAAAAGAGCTGCCCTCTCTCCAGCAGCCCAATGAACAGAAGGAAGGAAC
GCCAGCTCCATTGGGGACACAGCCATCCAGAACCTGAGTCC1GGAATGCAGGCCCAAGCACTGCCAACAG
SACCGGTCCCAAGGGGGCTGGGGCCACCGGCTGGATGGCTTCCCCCTGGGCGGCCCTTCTCCAGACATC
TGAACCAATCTGCCTTCCTAACCGTCAGCATGTGSTATATGGTCCCTGGAACCTACCACAGTCCAGCTA
CTCCACCTCACTCGCCAGGCTGAGACCTCAATTTCCTGGAGATTGATATTCGGCTGCTGCCACTGC
CGCAGCCACACAAACCGCTAGAGTGTGCCAACTTGTGTGGGAGGAAGCAATGAGCCGATTCTGTGAGG
CCGAGTTCTCGGTCAAGACCCGACCCCACTGGTGTGCACGCGGGGAGGGGCTCGGTTCTCCTGCTT
CCAGGAGGAAGCTCCCCAGCCACACTACCAGCTCGGGGCTGCCCGAGCCATCAGCCTGATATTTCTCTG
GGTCTTGAGCTCCCTTCCCTCCTGGGGTGCCACATTGGACAATATCAAGAACATCTGCCACCTGAGGC
CCTTCCGCTCTGTGCCACCCAACTGCCAGCTACTGACCCCTACAAAGGGAGCTGCTGGCACTGATCCA
GCTGGAGAGGGACTTCCAGCGCTGCTGCCGCCAGGGGAACAATCACACCTGTACATGGAAGGCCCTGGGAG
GATACCTTGACAAATACTGTGACCGGGAGTATGCTGTGAAGACCCACCACTTGATGTGCGGCCACC
CTCCAGCCCTACTCGGGATGAGTGCTTGGCGGTGGGGCTCCTTACCCCAACTATGACCGGGACATCTT
GACCATGACATCAGTTCAGTCACCCCAACCTCATGGGCCCTCTGTGGAAACCAAGAGTTCTCACC
AAGCATAAACATATTCCTGGGCTGATCCACAACATGACTGCCCGCTGCTGTGACCTGCCATTTCCAGAAC
AGCCCTGCTGTGCAGAGGAGGAGAAATTAACCTTCATCAATGATCTGTGTGGTCCCGACGTAACTCTG
GCGAGACCCCTGCCCTCTGCTGTACCTGAGTCTGGGATGAACAGGTCAACTGCTTCAACATCAATTAT
CTGAGGAACGTGGCTCTAGTGTCTGGAGACACTGAGAAGCCCAAGGGCCAGGGGAGCAGCGCTCAACTG
GAGGAACAAATATCAGCTCCACCTCTGAGCCCAAGGAAGAAATGATCAGCCACAGCCCTAGAGGGTCAAG
ATG

FIGURE 44

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FIGURE 45A

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GAAGATGGCTAGAAATGGTGCCTTTCTGAGTGTCTAAACTTGACACCCCTGGTAAATCTTCAACACACTT
CCACTGCCCTGCCGTAATGAAGTTTGGATTCATTTTAACCACTGGAATTTTCARTGCCGTCATTTTCAGTT
AGATGATTTTGCACTTTGAGATTAAATGCCATGCTATTTGATTAGTCTTATTTTTTATTTTACAGGC
TTATCAGTCTCACTGTTGGCTGTCTATGTGACAAAGTCMAATAAACCCCCAAGGACGACACACAGTATGGA
TCACATATTGTTTGACATTAAAGCTTTTGCCAGAAATGTTGCATGTGTTTTACCTCGACTTGCTAAATCG
ATTAGCAGAAAGGCATGCCCTAATAATGTTGTTGGTGAATAAATAAATAAGTAAACAAWAARAARAWGC
CTGCTCTCTCTGTGCCCTAGCCCTCAAAGCGTTCATCATACATCATACCTTTAAGATTGCTATATTTGGGTT
ATTTCTTGCACAGGAGAAAGATCTAAAGATCTTTTATTTTCATCTTTTTGGTTTTCTTGGCATGACTA
AGAAAGCTTAAATGTTGATAAAATATGACTAGTTTGAATTTACACCAAGAACTTCTCAATAAAGAAATC
ATGAATCCTCCCAATTTCAACATACCAAGAGAGGTAATTTCTTAACATTGTTCTATGATTATTTG
TAAGACCTTCACCAAGTTCTGATATCTTTTAAAGACATAGTTCAAAATGCTTTTGAATCTGATTTCTT
GAAATATCCTTGTGTGTATAGGTTTTTAAATACCAAGCTAAAGGATTACCTCACTGAGTCATCAGTACC
CTCCTATTCAAGCTCCCCAAGATGATGTGTTTTTGCCTACCTAAGAGAGGTTTTCTTCTTATTTTAGATA
ATTCAAGTGTCTAGATAAATTATGTTTTCTTAAAGTGTATGGTAAACTCTTTAAAGAAATTTAATAT
GTTATAGCTGAATCTTTTSGTAACTTTAAATCTTATCATAGACTCTGTACATATGTTCAAATTAGCTGC
TTGCCTGATGTGTATCATCGGTGGGATGACAGAACAAACATATTATGATCATGAATAATGTGCTTTGT
AAAAAGATTCAAGTTATTAGGAAGCATACTCTGTTTTTAAATCATGATAAATATCCATGATACITTTAT
AGAACAATTTCTGGCTTCAGGAAGTCTAGAAGCAATATTTCTTCAATAAAAGGTGTTTAACTTTAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 45B

CAAGAAATTCGGCACGAGGGCGTGTCCAGAAAGTGGTGGATAGTGTGAGTAGTAAATTCAGCTGGCAGGT
TCCCTGAGTGCAGCTGGCTCGATAGTCTGTAATGAAGAGTGTGTCCGAAAGACTTTGAATCCAGTATGAA
TGTAGTACAGGAAATTAATTTAGTCTAGGATCAGAGGGACTGAAGACTGGGCTCCTCCTAGATTTCAAA
TCATATTTAATATTCATCCACCACCTCAAGAGGGACCTTGTGGTGGCAGCCAGAAATTTTCTGTGCCGGC
TGTGGAACCTCCAGTAGAGCCTAAGTTTGTGAAGCGGCTCCGGTACTGCCAATACCTAGGGAAATTTCTG
TCACTGCTGCCACTCATATGCAGAGTGTGTGATCCCTGCCGAATCCTGATGATGTGGGACTTCAAGAAAT
ACTAGCTCAGCAATTTCTCCAAACAGCTGTCTGACAGCATATGSCACCAGCCCATTTTCAATTTGCTGAGC
ATCGGCCAAAGCCTGTATGCCAAAGCCAAAGGAGCTGGACAGASTGAAGGAAATTCAGSAGCAGCTCTTCCA
TATCAAGAAGCTGTGAGSACCTGTAGGTTTGTATACAGTGCATTAAAGGAGTTCGAGCAGGTGCCGGGA
CACTTGACTGATGACTCCAGCTGTCTCCCTTAGGACCTGGTCAGCATCAAGAAAGGCTGTGGCACCTT
TACTCAAGGACATTTCTGAAGCTTCCCTTGCACATGTGCTGGCTGTGAGCTGTGTCAAGGAAAGGCTTT
ATTTGTGATTTTCCAGAAATACGACTGTCTATCTCCCATTTTCAGACAGCAACATGTAGTAGATGTTCAGC
GTGACGGGCTTGTCTTACAAACAGTGTCTCCAGTCTCCGAGTGGCCCGGTGTGCSAGGATCAACAGCGA
GGAGAAAGCTTCTGGAAAGTGTGGCCTCTGCAGCAACATGATGCCCTGAGTACTGTGAAAAAGACTGTTC
AACATGCCCTTATGATAACACCGATTTGTGTCTATTATTGGTGACATTGTTTAGATATTGGTATTGTATA
TTAAGGAAAGAGATGGTCTATATTCTCTTTATTGCAATATACTTAATGTTTCAAAAGAAATGCAGATTCTGTG
TTAAGCACAGGCTGATAGTGTGTGTTTGTTTACAAATGTTCTGTTTGGCTGCTATTGGTTTTTAA
GAGGTTTTTTTACTTTTGTATTTGAATAGTTATGTTTCACTGATGCTGAGCCAGTTTGTATGTGTGTGCA
TATATGTGAAGTGTAACTGACAAAGATGAATTAAGTCTGCTTCTCTCTTAAGCTTGTATTGATGAAGTGT
GTTGGTCTTTCAAGTGMANAAWATATGACCCCAAAAAAAAAAAAAAAAAAGCAATGCGAAGGTG
CTAATCCTGACGCTCGTGGTGGCCGCTGCGGCTTCGCTCTGAGCAGCAATGGGCGCAAAAGGAAGAA
CGAGGCCCTCGCCCAACGTTGTCTGACGCCGAACCCGCG

FIGURE 46

GGAAATTATAGATCTTGATATTGAATCCATCAGTGATTCAAGAGATACACCTATTTCCTAAAAACACCTA
ACATGATTTGGTTATGGAATCATGTGTGGATAGGTCTTAAAGACTGTTCCTCAAATCTTGACACAGTT
TTCAGGGGTGGCTTATTGACTTGACCGGTTGGGCAGATAATCCAGATTACCTAAGATTGGGTAAAAAGT
CATCTGTGACTTGTGGCAGGGCATTGCTAAGTGGAGTACAGGATCTAAAGGGTTTTCTTAGAAAGGG
CAATATTGTCCAATGAAGTAAGCAGAGGACTCTGGGTTAGAAGCATCTGCACAAAACTGGTGAGACCTA
CTCTCCACTGCTCTGCAGCTGGATGGCTGATGGCAGGCTGAGCAGTGGGGAAGCAGGTTTTAACACAGGG
AGTCTTCCAGGTCAGTGTATATTGAGAAACATAAACTATTGTCTGTACATTCCGAGGTGAGCCTT
CTCTTTACGTTTTATAATATGCAATGCCAGCTTCTGGAAGCAAGTATCATCATGTACCAATGCTTTA
TACACCATCAGTTTCAATGAATTTTATGATGGTCAAGCTTGTGTAATATGTCTCTTAGATGATTTTGG
GGAGATGTGATTTATTTTATATTTTCAAAATGCAATTCATTTCAATAAAGTTATCTATTGAGCAAC
GAAAAA

FIGURE 47

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AAATTTTGGCCCCCTCCGAGGCCCAAGAAATTTCCGGCCACCGANGGAATTTTGGTACCCACCCAGGGGG
GGAATGGAATGCTGCTTTCAAAACTTAGTTTCTTCCATTTTCTCCTAGTCTGGCCCTTGACACAAAT
CTGGTAGAAAGAGCCTATAAATTGAGGGCACTTGTACCCCTCCCTGTGCCCCAGAAAGTTCTTGGAGAG
AAGTGCAAGAAATTTGTAACACGGCCGCTGAGGGCCGCTGATGGCCATGGGCTGGGCTCCGTATCAGGC
CTGCTCACCTTGCTGGGAGCTTTATTCGTATCTCATTTTGAATGTCCAGAGGGAGCATCAAAAGAGCCCA
CAGCTCCGATTTCCAAAGAGTGATATTGACATTTATGGAGATTGGTGTGTAACATATTTTGATAAAATCT
AACTTATTTTGGTTGGGCTTTGGTTGTCTCTTGTCTTAGGACCTGGTAGTTATTTGCTTGATTTTTTTTC
CGTTATTTTCTACATAGGCCAAAGAGAATTCGAGGGATAGACAGTCTCCAAAGAAAAGTGAAGTGGTGGGAGA
GAATTTGCTTTTCTTTTCTTTTCTCTAGTTTCTTTCTGGCTGAGATTTCCTGGCAAGACAGCAC
CCAAATAGACTATTTAGAGTTGACATTTGACATTTTAAATGGGCGCCATGGCTCATTTTGTAGATTGAGAAGG
TGCCTCTCCCTGCTCCAGTCTCATCATGACAGCGTGTGACAGCTGGGAGTCTGTGGCCTTCTCAGGC
AGAGGCTTAAAGCTGGACACAAAGCACGCTAGGCTGGGAGGGATGGGACCCATGCCCTCTCTTAGA
GGAGCGGCTTCTGGTTAGGAAAGGACAGCTGGGGGTGCTTGCATAATAGTTCACTGGTCACCTGCTTT
TATGAGTAGTGTITTTGTGCACTTGCCAGGGTTTCTCTCTGTGTGCGAGGGGAGTGATTAAGCAATGG
TGTCTGGAGTAGGCTTACAATTTTAAATAGACTTTTCTTATCATATCCCTCATTTCTTCTCCCTGAATAA
AAATACACACAAAGCAAAATAATGATAGTTTACATCTCTTAGTTCCCTTGCCCAAAACAGAAATATCT
TAGTTCCACTGGCCAGGATTTTCTACATAGTCAGAACTTACACATTACTAGAGGCACACCCACCAAGGAG
TATTGTGCTCACTTTTATCTGTGACACAGCCACAAATACCCACATTGGAAGAGCCCATTTGTGATGGGTAA
ACATCTCCTTCTGCTGCCACACACCTTGTGACTGCCCTGCTGTGTGTGATGACCTCCGAGGGCCCTAAT
CATGAAGCAGCAAAACCCAGCAGATCTCCACCCCTGCTCAGGAGCTCTGCTGAAGAGGGGATGAAGTG
GGTCTCCAGGGAGGCAUTGGGGGCTTGTGGCAGCTGGCTCGGGAGCCGGCTTACAGGAGGGCAGCTCTG
CAGTTGGGAGGGGACCGCTCCGAGGAGGACAGGCTCTACACACCCCTCTACTTATCATCCCTGCT
CACACACCCCTTGTCCAGGCTTTATGCAATCGGATTTATTTTCCAAATCGAGAGGACAGTGATAGATGCA
TTTCCCCAGGCTGTCTCAGAAAGGCTCCATAATGTATAGTTGTGTCAGAAATGCTGAGATCTCCCCCACT
TTTGGTTTTTGCAGCAGTAAAACTCTTTCCACTGTGACTTATTTTCTCTCTCAGGACAGCCAGCTGG
TCCCTTGTGCTGACTCTAGCACAGTGGCCAGGATCCAATACGAGTCCAGGGGTGACCCGAGGATGGTGGG
GCAGCGGGCTTCTCACCTACCCAGCCACCAAGGCTGACGCACTGCTCCTGCACTTTCAGCAGATCC
CTGTGCAAGCTGGAGGGGTGATGGCCGCTCACCTTTGTTCAGATGGGTGGAAACGCTGATGATACAG
CTCCCTCCCTGCCGTGCCCTGCCACGGAGCAGGCTTGTGAACGTGGCTGGTGTTCAGTCCACGTTGGCA
TGGCTTCCAGCCCAACCCACAGTGGAGACTGGAGACAGGCAATGATCTGGTGGGGGACGTTGGACATG
CCCCATAGGGGCCCCACCCAGACTTAACAGGCAAGGTCTGGGCATTGCCGACGAGGACTCAATGCTAA
ACCAAGCCTGCTGCTCTGTGCCAGGGCCCTCTCTGATTTACACATCCATTTTACACAGACCCCTTC
CTTCTTAATAAGGCTGACAGTTCTGTGGCAGCCAGAACCCACACCATGAGACAGGGAGTGGGGGCC
TTTGTGCCCAACTCCAGCACACCTGCGTTCTGGGGTGTGTGAGAGGCAATGTCGTCTGTGGCTGGTGG
TCTCTGTGACAGTTCCGAGGACGGGGAATTGCAAGGGTGGTGGGGGCTGAGGCTTATATGTGGAAGTGA
TGCAGAGTTCCGCTGCAAGCGGATCTGGATATACACTATGTATAATTTGTACGTGTAATTTAAATATATC
TGTTTGCCATCGTCATGAGAAGATTATATGAAGGCTCTGAAGGGAGAGGGAGATGTACATTTCTGCCAGGC
TCTTGGGCACTTAICGAGTCAATGAATTTGATGACTGTGATCCAGTGGTGCAAGAGCTACACTCCATG
TGTCACTACGCTTATGACTCTAATGTATTTTAAAGCAAAAATGTACCCGACTCCATCTTCAACCCCTC
GATTTCTCGAGTCCAGCCTTTCTGTGCCAGTGTCTACTGAGCCACACGCTCTCGCCATCGGGACCCGGC
TGGGCTCGAGTCTCGGGGACAGTTGCCATGGAGCCCTCCTGGGTCTTCAAAATGTGCTGAGTGCCA
GCTGAATAACCCACAGGAGATGAGTACCTTGGCCAGCTTAAGAGAGATTTTCTCAGGGTATTTATTA
GTGTGTCCAGCAGGGTCAAGGAGCAGGATGGAAGATGCATTGAGCTGTTAATTTATTAACAGGCAAAAT
GATTTTGTGTTTCTTGTGACAGACTATTAAGTTTGGGACTTATTTCCCATTTGAGAAGTTATAATATAT
ATTTAAGATGATAGTTTCTGCTTAAGTTTGTGCTTTTCAAGCTTCAATGAGTTTAAAGGAGCACTAAGGGTA
ATGATACCAATGAGGGTTGGTTTATATCAAACTGAATAGCTGTGGTTTCTCCAGTAAATATTTCTCTCT
ACTGAACATGGAGCCATTAATAGAGTTGTGTGTTTTTATATGTACATTTGTATATTTTGTGCTTGT
TGTGTTCTATTTTCTAATAGTTTCTTTTGTGTTCTTAAAGTTGTGATAGTATAGATTAGATTCTGATGC
TAACTGCAAAATCAGGTTGCTCTGCTGGGTCTCTCTGCTTTTATTTTACTTAAAGGACAGTGTAGTTG
TGGTCCACCACTTTCAAAAATGTGAAGTGGCTGCTCCCTTTTGTGTCAGACACTGTGTATCTG
AGCACTTCTACCACTTTATGTGTGAAAATCAAACTCTTTGTGGTACATTTATCTCATGCTTCTGCAAA
TTCGANTAAATCTATGGCTTCCAAAAAAGAAAAAAGAAAAA

FIGURE 48

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